

1001

```

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGcGg actTTCTTcc
551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CAtcgTACAT
601 ACCCTcgtCT TTTTcgTTtt CAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTACCCTG TTTTATTTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGGCC TTTGGAACCC CGAACACCCG GGATTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTCAATAT GGCGGGCGGC GATGCCAAG
401 CCTTGATGAC GGGTTCCTTG TTTCAATCGC TGCTGGCGGT TTCTATGGGT
451 TCGGTATCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLVSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

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a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX  
190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq  
1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT  
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC  
101 ACACATGGAT TTTACGTTCG GTCAGGCGGC TCAATACCAA CAGGCCGCGT  
151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG  
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA  
251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT  
301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC  
351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep  
1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRLNTNRPR  
51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP  
101 D\*IRLRRTFS LLNFASASGT \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq  
1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT  
51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCCTTAC  
101 AAACATGGAT TTGCGTTCG GTCAAACGGC TCAATACCAA CAGGCCGCGT  
151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG  
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA  
251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG  
301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC  
351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep  
1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQWILRS VKRLNTNRPR  
51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP  
101 DWIRLRRTSS PLKFASASGA \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m628/g628** 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQTWILRSVKRLNTNRPR	LKSSAASLIM			
g628	MCVPLKPAGCGPPNSCVSILAAFS	DGTSAPAAALHTWILRSVRLNTNRPR	LKSSAASLMM			
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGA				
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGT				
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

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a628.seq  
 1 ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT  
 51 TTTCGATGTG GCAGCATTTC CAGACGGCAC GTCTGCGCCA GCTGCCTTAC  
 101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT  
 151 CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGCT CTGCCGCCAG  
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA  
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG  
 301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGC  
 351 TTCGGGCGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

a628.pep  
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALHTWILRS VKRLNTSKPR  
 51 LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP  
 101 DWIRLRRRTSS PLKFANASGA \*

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRLNTNR	PRLKSSAASLIM		
a628	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALHTWILRSVKRLNTSKPR	LKSSAASLIT			
	10	20	30	40	50	60
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRLRRRTSS	PLKFASASGA			
a628	TTGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVAVHKPDWIRLRRRTSS	PLKFANASGA			
	70	80	90	100	110	120

m628.pep X  
 |  
 a628 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

g629.seq  
 1 ATGACTGCca aacCTTTTTT CCTCAACCTG GCcaaCCTCC TGCTGCCggc  
 51 ggtatTGTTT GCCGTcAGcc tGtcggTCGG cattgccgaT TTCCGCTGGT  
 101 CGGATGTGTT TCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC  
 151 CTGCCGCGCA CGTTTGcgaT TGTGTTGACG GGCgcgtcga tagcgGtggc  
 201 gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTtcta  
 251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg  
 301 ctgctgcctg CcgGccgct gccggTcaAA ATGTCGGtag Cgcgcgttgc  
 351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaataccgC Cgcctgccac  
 401 cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG  
 451 GttgaGGCGG TGGCAGCGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAT  
 501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT  
 551 ACGAGCTGCT TTGGATTACG GGCGGTTTGG CGGTGTTTGC CTACCTGATT  
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATTT  
 651 GGGTTTGAAC CGGACGGCGG TGTGTGGTGC GGGTTTGATT ATTGTGGCAC  
 701 TGATTACATC GCTGGTCATT GTAACGGTCG GCAATATTCC GTTTATCGGG  
 751 CTGGTCGTGC CGAATATCGT CAGCCGCCTG ATGGGCGACA GGCTGCGCCA  
 801 AAGCCTGCCT GCGGTCGCCC TCTTGGGCGC GTCTTTGGTT TTATTGTGCG  
 851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTCC GGTCTCCACG  
 901 GTTTTTGGTG TGTTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA  
 951 ACCCGCCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

g629.pep  
 1 MTAKPFSLNL ANLLPAVL AVSLSVGIAD FRWSDVFSLS DSQQVMFISR  
 51 LPRTFAIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLMSL  
 101 LLPAAPLPVK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGXIFGGV



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151 VEAVATFVAY EFEMLQMLGV WQQGFSSVL LGRYELLWIT GGLAVFAYLI  
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG  
 251 LVVPNIVSRL MGDRLRQSLP AVALLGASLV LLCIDIIGRMI VFPFEIPVST  
 301 VFGVLGTALF LWLLLRKPAY AV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

m629.seq  
 1 ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC  
 51 GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT  
 101 CTGATGTGTT TTCACGTGCC GACAGCCAGC AGGTCATGTT CATCAGCCGC  
 151 CTGCCGCGCA CGTTTGCGAT TGTGCTGACG GGCGCGTCGA TGGCGGTGGC  
 201 CGGCATGATT ATGCAGATT TGTATGCGCAA CCGTTTGTG GAACCGTCGA  
 251 TGGTGGGCGC AAGCCAAAGC GCGGCTTAG GTTGTGCTGCT GATGACCCGTG  
 301 CTGCTGCCGG CCGCGCCGCT GCCGCGGAAA ATGTCGGTTG CCGCCGTTGC  
 351 CGCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC  
 401 CGACCGCGCA ACTGATGGTG CCTTTGGTGC GGATTATTTT CGGCGGTGTG  
 451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAT  
 501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGGCGGT  
 551 ACGAGCTGCT TTGGATTACG GGCGGTTTGG CCGGTGTTGC CTATCTGATT  
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT  
 651 GGGTTGAAC CGGACGCGCG TGTGTGGTC GGGTTTGATT ATTGTGGCTT  
 701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG  
 751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATGGGCGACA GGTTCGCCCA  
 801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG  
 851 ACATTATCGG ACGCGTGATT GTGTTCCGT TTGAAATTCC GGTCTCTACG  
 901 GTTTTGGTG TATTGGGTAC GGCTTGTTT TTGTGGCTTT TGTGAGGAA  
 951 ACCCGCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pep  
 1 MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR  
 51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMVGASQS AALGLLMLTL  
 101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIIFGGV  
 151 IEAVATFIAY ENEMLQMLGV WQQGFSSVL LGRYELLWIT GGLAVFAYLI  
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG  
 251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFEIPVST  
 301 VFGVLGTALF LWLLLRKPAY AV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRRLPRTFAIVLT					
g629	MTAKPFSLNLANLLLPVLFVAVSLSVGIADFRWSDVFSLSDSQQVMFISRRLPRTFAIVLT					
	10	20	30	40	50	60
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQS AALGLLMLTLLPAAPLPAKMSVAAVAALI					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQS AALGLLMSLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQS AALGLLMLTLLPAAPLPAKMSVAAVAALI					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQS AALGLLMSLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMLQMLGVWQQGFSSVL					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLQMLGVWQQGFSSVL					
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMLQMLGVWQQGFSSVL					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLQMLGVWQQGFSSVL					
	130	140	150	160	170	180
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
g629	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
g629	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					

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g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VTVGNIPFIGLVVPNIVSRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```
a629.seq
  1  ATGACTGCCA AACCTTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
 51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101  CGGATGTGTT TTCGCTGTCT GACAGCCAGC AGGTTATGTT CATCAGCCGC
151  CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GGC GCGTCGA TGGCGGTGGC
201  GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTGTCT GAGCCTTCTA
251  TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTTGCTTCT GATGTCCTTG
301  CTGCTGCCTG CCGCGCCGCT GCCGGTCAA ATGTCGGTTG CCGCCGTTGC
351  CGCGTTAATC GGGATGTTGG TGTATTATGAT GCTTATCCGC CGCCTGCCGC
401  CGACGCGCGA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451  GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAA
501  GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTCGGACGGT
551  ATGAAGTGTG GTGGGCAACG GGGATTTTGG CTTTGTGTTG CTATTTGATT
601  GCCGACCAGC TGACGATTTT GGGTTTGGG GAAACGGTAA GCGTGAAGTT
651  GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701  TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751  CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGGCGACA GGCTGCGCCA
801  AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851  ACATTATCGG ACGAGTGATT GTGTTCCGT TTGAAATTCC GGTATCGACC
901  GTCTTCGGCG TATTGGGTAC GCGGTTGTTT TTATGGCTTT TGTAAAGGAA
951  ACCTGCTCAT GCCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```
a629.pep
  1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
 51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMLSL
101  LLPAAPLPVK MSVAAVAALI GMLVFMMILIR RLPPTAQLMV PLVGIIFGGV
151  VEAVATFIAY ENEMLQMLGV WQGDGFSGLV LGRYELLWAT GILALFAYLI
201  ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251  LVVPNIISRL IGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301  VFGVLGTALF LWLLLRKPAH AV*
```

m629/a629 95.7% identity in 322 aa overlap

```
           10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
           10      20      30      40      50      60

           70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLLPAAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a629      GASMAVAGMIMQILMRNRFVEPSMAGASQSAALGLLMSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120

           130     140     150     160     170     180
m629.pep  GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMLQMLGVWQGDGFSVSL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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a 629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAAYENEMLQMLGVWQQGDFSGVL
              130      140      150      160      170      180

              190      200      210      220      230      240
m629.pep   LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
              ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
              190      200      210      220      230      240

              250      260      270      280      290      300
m629.pep   VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
              250      260      270      280      290      300

              310      320
m629.pep   VFGVLGTALFLWLLLRKPAYAVX
              |||||:|||||
a 629      VFGVLGTALFLWLLLRKPAHAVX
              310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccattgt tttacggcat
51  gtacaacgtc GGCGCACAGG CATTCGGTGC CTTAACGCCC GAtttgctgc
101 aacaaagcat cggccacgac ggcaattacg ccctcgccaa cgctttgggc
151 atcaatatgt cccccgaaGc gggcgtgtTg ggcaaatgc tgttcgGCGC
201 GATttacttc ctgccgattt acgcgaccgt aTTTATTGTG GGcggcttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAC ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGC
451 GCCTTCCTGT TCTTCGCCTA CCCCGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tCGctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 cttggtagat ggcacttggt GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQQSIAHD GNYALANALG
51  INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFA VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLEFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVTGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFFVF ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GGCGCGCAGG CATTCGGTGC GTTAACGCCCT GATTGTGCTGC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GACAAAATGC TGTTTGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACTGT ATTTGTTGTG GGCGGTTTCT
251 GGGAAAGTTT GTTCGCCACC GTGCGCAAAC ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCTTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG
701 CTTCTTGCGG CATTATTGCC GCGGTGATGA TCGGTATGAT TCGCATGTCT
751 TCGCTGTTC AACTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC

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1008

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801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTGTT CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep

```

1 MMILVWLALF PAMFYGMYNV GAQAFGALT DLQONIAND WHYAFANALG
51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

      10      20      30      40      50      60
m630.pep MMILVWLALFPAMFYGMYNVGAQAFGALTDLQONIANDWHYAFANALGINMSSEAGVS
          |||||  |||||  |||||  |||||  |||||  |||||
g630      MMILVWLALFPMPFYGMYNVGAQAFGALTDLQQSI AHDGNALANALGINMSPEAGVL
          10      20      30      40      50      60

      70      80      90      100     110     120
m630.pep DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
          |||||  |||||  |||||  |||||  |||||  |||||
g630      GKMLFGAIYFLPIYATVFIVGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA
          70      80      90      100     110     120

      130     140     150     160     170     180
m630.pep ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
          |||||  |||||  |||||  |||||  |||||  |||||
g630      ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
          130     140     150     160     170     180

      190     200     210     220     230     240
m630.pep QWAAHGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
          |||||  |||||  |||||  |||||  |||||  |||||
g630      QWAAHGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA
          190     200     210     220     230     240

      250     260     270     280     290     300
m630.pep GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
          |||||  |||||  |||||  |||||  |||||  |||||
g630      GVMIGMIAMSSLFNFIGSDTKAMFAM----HLVHGTWVKDDYHSLYIK.
          250     260     270     280

      310     320     330     340     350
m630.pep YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq

```

1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51 GTACAACGTC GGCGCACAGG CATTCCGGTGC GTTAACGCCC GATTTGCTGC
101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGC AAAATGC TGTTGGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
251 GGGAAGTTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
301 TTTGTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCA GCCTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTA AAACCTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCA TAACCGGTCA AACCATCACT
601 TGGATGGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGGCTT TATCGTGTTC GCCCGCATCG

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1009

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTG
1001 CCCCATTTC CGACTATTTT GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

a 630.pep

```

1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLTVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIAN	WHYAFANALGINMSSEAGVS				
a 630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQOSIAND	WHYALANALGINMSSEAGVL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYFLPIYATVFVVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
a 630	GKMLFGAIYFLPIYATVFIV	GGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPAN	LSGDAVWTAVDGYSGATALA				
a 630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPAN	LSGDAVWTAVDGYSGATALA				
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
a 630	QWAAHGADGLKNAITGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYH	LVGGFAIGMLFMATDPVSASFTNVGKWW				
a 630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYH	LVGGFAIGMLFMATDPVSASFTNVGKWW				
	250	260	270	280	290	300
	310	320	330	340	350	
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAP	IFDYFVAQANIKRRKARSNGX				
a 630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAP	IFDYFVAQANIKRRKARSNGX				
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

g635.seq

```

1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTGAAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA

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1010

301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC  
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AACATCGGT  
 401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

g635.pep

1 MTRRRVGKQN RIAIHSAYR KMVVFVFIQI HDDGDFQLRE LFERQGIQFR  
 51 LKTQIGHNAP HILKRRALHF LTQFFQHFF RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IPRFPTLQF DFSVNNRIIV KHRCISQITIR QGSVPD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC  
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG  
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC  
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGC  
 201 GCATCTGCTC CTTATCCAGT TTTTAAACA CGTCTCTTC CGTCAGCTTT  
 251 TGCCCGTAAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGGA  
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC  
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFIQI HDDGDLQLCK LLERQGIQFR  
 51 FKTIQIRHNP HILKRRGHLL LIQFF\*HVLV RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D\*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFIQHDDGDLQLCKLLERQGIQFRFKTIQIRHNP					
	10	20	30	40	50	60
g635	MTRRRVGKQNRIAIHSAYRKMVVFVFIQHDDGDFQLRELFERQGIQFRFKTIQIGHNAP					
	70	80	90	100	110	120
m635.pep	HILKRRGHLLLIQFFXHVLFRLLPVKIVQKRRHRSRPAGKIQILLYNIEIAPFFPTLHF					
	70	80	90	100	110	120
g635	HILKRRALHFLTQFFQHFFRQLLPVKIVQKRRHRSRPAGKIQILLYNIEIPRFPTLQF					
	130					
m635.pep	DFSISNRIIVDX					
	130					
g635	DFSVNNRIIVKHRCISQITIRQGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC  
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG  
 101 GGGATTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC  
 151 CTCAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC  
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCTCTTC CGTCAGCTTT  
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA  
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC  
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFIQI HDDGDLQLCK LLERQGIQFR  
 51 LKTQIRHDAP HILKRRALHL LIQFFQHVLV RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D\*

m635/a635 95.4% identity in 131 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

1011

```

m635.pep    MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHNAP
             |||||
a 635       MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHDAP
             10      20      30      40      50      60

             70      80      90      100     110     120
m635.pep    HILKRRGHLLLIQFFXHVLFQRLLPVKIVQKRHHRSRPAGKIQILLYNIEIAFFPPTLHF
             |||||
a 635       HILKRRGHLLLIQLFQHVLFQRLLPVKIVQKRHHRSRPAGKIQILLYNIEIAFFPPTLHF
             70      80      90      100     110     120

             130
m635.pep    DFSISNRIIVDX
             |||||
a 635       DFSISNRIIVDX
             130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGTtgGc atTGTAGGCA AAAACGCACT
51  TGCCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGCGCGC TGTACGGCTA TGGTACGCCC GCTCTGTGTC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CCCCCGCCG
751 GGCGCGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCCA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCAGC
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCCGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCTGAAA CCGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDAI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGNNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIVFENQG ARGGFEINT GIHCWQAHTG TNGNQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCCG TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCG
201 AAATATTGCC GCTGATTTTC CTGTCTGTTG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTTC TAGGTGTTGT GCGTGCTGGT
301 ATTTGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCAGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTTCTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGCGCGC TGTACGGCTA TGGTACGCCC GCTCTGTGTC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CTTCAATCG TAATCGGTTT GTCATGTGTA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CCCCCGCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

1012

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

```

m638.pep
  1  MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
 51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVRAG
101  IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151  RTMQIYADRI IQNIVFVNQG ARGSF FEINT GIHCGQAHTG TGNGQVAERY
201  VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251  GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

      10      20      30      40      50      60
m638.pep  MIGEKFIVVGIIIGKYALACLVDNVVVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI
g638      MIGGQFIVVGIVGKNALARFVDNIVVNIGIVDIVEHDALIAAADGDIVEHFEPFGKHQHI
      10      20      30      40      50      60

      70      80      90      100     110     120
m638.pep  AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFGVVRAGIGKNAVPPFGNVVADDLRTG
g638      AHIVAHGNIAADFAVVGVIHVDGETQVAEAVVFIGVVRAGIGKNAVPPFGNVVADDLRTG
      70      80      90      100     110     120

      130     140     150     160     170     180
m638.pep  CVPNGNAVAAALVHAQSRVADDFILAHHRIGRTMQIYADRI IQNIVFVNQGARGSF FEINT
g638      RVPNGNAIAALIHAQGRIADDFILAHHRIGRTMKVYAERI IKNIVFVNQARGGFEINT
      130     140     150     160     170     180

      190     200     210     220     230     240
m638.pep  GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCCTVGRPFNRNRFVNVKFGFIYA
g638      GIHCWQAHTGTGNGQVAERYVRRVYGYGTPALVPFDGCGTVGRPFNRNRFVDIKFGLIYA
      190     200     210     220     230     240

      250     260
m638.pep  GSQFERIARPGAGKCGIPISIIGSX
g638      GSQFDRIARPGAGKNFGKVVLRGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF
      250     260     270     280     290     300

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

```

a638.seq
  1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
 51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101  TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151  TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGCG
201  AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251  AAACGCAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301  ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351  GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTACAG
401  CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451  AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501  CAATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551  GCGGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601  GTCCGCGCGG TGTACGGCTA TGGTACGCC GCTCCTGTCT CCTTCGATGG
651  TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
701  AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751  GCGCGGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

```

a638.pep
  1  MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
 51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
101  IGKNAVPPFG NIVADDLRTG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151  RTMQIDADRI IQNIVFVNQG ARGSF FEINT GIHCGQAHTG TGNGQVAERY
201  VRRVYGYGTP APVSFDGCRV VGRPFNRNRF VDVKFGGLIYA GSQFERIARP

```



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251 GAGKCGIPIS IIDSW\*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGKEFIVVGIIGKYALACLVDNVVNI GIVDIVEHNALIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIVGKNALARFVDNVVNI GIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFAVVGVHIVDGETQIAEAVVFVGVVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFAVVGVHIVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNIVADDLRAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQGARGSFFEINT					
a638	RVPNGNAIALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQGARGSFFEINT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCGTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGCRTVGRPFNRNRFVDVKFGLIYA					
	190	200	210	220	230	240
	250	260				
m638.pep	GSQFERIARPGAGKCGIPISIIGSX					
a638	GSQFERIARPGAGKCGIPISIIDSX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTGGGAA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTTCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGCGGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GCGGGAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSVSGN ISVGNNMGVY LMFSERLKVF DNIAGVSRD*
151 GIMLNYYVNS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGD SAYRPDG IIDQIIWRAP VSRLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

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## m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGCCTC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGA
201 CGCACCCGGT GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCGAG ACGCACAACA CCTACAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCTTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGCTCTT GCATGACAA TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTCAGCA CGCGCTTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGCG
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGGCAG GCGGGAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

## m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDEISGN ISVGNMGGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNHYVNS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLDHN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNG IIDQIIWRAP VSRLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMGGYVLMFSERLKVF DNIAGVSRDXGIMLNHYVNSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGGYVLMFSERLKVF DNIAGVSRDQGIMLNHYVNSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTA AIEGTSLDHNSFINNGSQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTSLDHNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSDAYRPDGIIDQIIWRAPVSRLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDAYRPNGIIDQIIWRAPVSRLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLEKETV RQSEWGRAENGSLN					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLEKETV RQSEWGRAENGSLN					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

## a639-1.seq

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```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAC TGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGCGCTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTGC TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTC GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTTCCTTA CAATGCCAAC TACGATAAAC
551 TGTCGCCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTACGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
751 TTCGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAA TTTCCCGCCG TTTTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGAAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNNMGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLN YVNYS DIHDNIINKA GKC VFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTS LHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPN IIDIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

a639-1.pep	10	20	30	40	50	60
	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	70	80	90	100	110	120
	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	130	140	150	160	170	180
	ISVGNNMGYVLMFSERLKVF DNIAGVSRDQ GIMLN YVNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNNMGYVLMFSERLKVF DNIAGVSRDQ GIMLN YVNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	190	200	210	220	230	240
	YDKLSANHFENCQIGIHFTA AIEGTS LHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTA AIEGTS LHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW					
	190	200	210	220	230	240
a639-1.pep	250	260	270	280	290	300
	NSAFDLNGDGF GDSAYRPN IIDIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV					
m639-1	NSAFDLNGDGF GDSAYRPN IIDIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	310	320	330	340		
	DSKPLMKPYAPKIQTRYQAMKDGLLKKVET RQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1   ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTGCA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501 GCGCGCCGGC GACATCATCA GcggTGCgAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCACG CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTGTGA TGTTCCTTGT GTCAGCCAGC CTTCCATCGG TAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAGT TTCTTGGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTTGACGGT GCGGAGCCGT GGCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1   MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNDSIQRS YKVIANQYRL
201 GSDKALQTAS ASDVREAAPA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGSYVRGGI FDRIEMIQGE
351 NSFRTDAQH ERVVELSAAD APRFKEVSF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1   ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1   MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK					
	:     :     :     :     :					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
                |||||||||||||||||||||||||||||||||||||||||||||||||||||:|
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAN
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||||||||||||||||:
g640          DGTIAGAKLVDHHEPIMLIGIPQSRVDFIDKYIGLNFINKPPTPSVAPGDIISGATVTL
                130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATGTG
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

                10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAAFVFLTAALPAYAERLPDFLAK
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAAFVFLTAALPAYAERLPDFLAK
                10      20      30      40      50      60

                70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
                ||||| |||||:|||||||||||||||||||||||||||||||||||:|
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAK
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                ||||||||||||| |||||
a640          DGTIAGAKLVDHHESIMLIGIPH
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GCGGTTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG TGTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTCG AGGGCGCAGG CGTCGGTCAG GGTGTGTTC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301 GGcaaagcgG ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CCGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGGCGGc gTAAGTGTAT
551 TCCGTGGCGa ggTTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCGG
651 AAACCTGATG GCGGCGTTGG ATTTGCGCGC GTTCGTAATC GACGAATCTG

```

1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATACGGCG
851 GTTGCAGGCA TTTCCGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCCGAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTGCGGGC
1051 GttgACGTAA ATGGTTtgtt cgtcggata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAt cgCgcgcgcg gaggtTtcgg gttcggtaAc gcccaaacgg
1151 cggcttttcgc ctTTGAAAAT CATGTCCAAA CCTTGTGCGA CTTCGccttc
1201 gccgcggaac tCTTGACAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

g642.pep

```

1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVQQEGC
51 GVVFVFLLYED KKS GDDFADE DFLQAGVVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLV FVQLN ACFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVS AFKTLRA QEFLQHLRGG VSVFRGEGFD DVLRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFHN
251 AVRHADQLQA AADKDV LERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVGI FVAGLHFACN RRAGGF GFGN AQTA AF AFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

m642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGCGGAT KTCGTT CAGC AGGAAGGCTG CGGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACTTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTTCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCGCG
601 GATTTTCGCG CGTTCGTAAT CGACGAATTT GATGTCGTTG CCGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTGTCAGGC ATTTGCGCAT
801 CGATGCGGTT GACGGCGTAA CCGACGGCGC GCAAGCCTTC GCGTCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CTTTGA AAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTGCAGT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

m642.pep (partial)

```

1 ACRRICLPEA ISAVQYIFAD VVQQEGCGVF VFLRYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADV SFQI FKDV FHNVR HADQLQAAAD KDV LERAQDTG
251 SVALGEFHG GCRHFGIDAV DGVT DGAQAF GCEGFAADV FGDQLQQVDDF
301 GEFV FALFG GN EEEVALRV ALPVFRGVDV NGLSVDIFV GLHFACNRRR
351 GGF GNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQR F D A G T Q R N G H
401 AVMPRNP

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep		10	20	30	
		ACRRICPLPAISAVQYIFADVQQEGCGVFVFRLYED			
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADVQQEGCGVFVFLLYED	10	20	30	40
		50	60	70	80
m642.pep	KESGDDFADKDFLQAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVVFVQLH	40	50	60	70
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLVVFVQLN	70	80	90	100
		110	120	130	140
m642.pep	ACFFFFGGGADKLNVNFGIKHIVRAFKNREGADVDSIAGGVSAFKTLRTQEFQLHLRGG	100	110	120	130
g642	ACFFFFGGGADELNVNFGIKHIVRAFKNREGADIDGDIAGWVSFAFKTLRAQEFQLHLRGG	130	140	150	160
		170	180	190	200
m642.pep	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVADV	160	170	180	190
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDESDIVADIS	190	200	210	220
		230	240	250	260
m642.pep	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQTSVALGEFHHGGCRHFGIDAVDGVTDGA	220	230	240	250
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQTSVAPGEFHHGGCRHFGIDAVDGVTDGA	250	260	270	280
		290	300	310	320
m642.pep	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGNNEEVALRVALPVFRGVVDVNGLSVDI	280	290	300	310
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGNNEEVALRIALPVFRGVVDVNGLFVGI	310	320	330	340
		350	360	370	380
m642.pep	FVVGLHFACNRRAGGFGFGNTQTAAALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQR	340	350	360	370
g642	FVAGLHFACNRRAGGFGFGNAQTAAAFENHVQTLCDLRFIAELLQRLQHQRAFDAGTQR	370	380	390	400
		410	420	430	440
m642.pep	NGHAVMPRNP	400			
g642	NGHAVMPRNPX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

1	GCCTGCCGCC	GTATTTGCCC	GCTATCCGCA	ATATCGGCAG	TCCAATATGT
51	CTTTGCCGAT	GTCGTTACAG	AGGAAGGCTG	CGGTGTCTTC	GTGTTCCGCC
101	TGTACGAAGA	CAAAGAGTCG	GGCGATGATT	TTGCCGATAA	AGACTTTTTG
151	CAGGGCGCAG	GCATCGGTCA	GGGTGTGTTC	CTGCAGGAAG	CTGCGGATGT
201	CTTCGGGCAA	AGTGTAGTCG	CGGGCGACGG	CGGCAAAGCG	GGCATCGGTT
251	TGCAGGCGGT	CGAGCAGGGT	TTGGTTTTTG	TCCAACCTCA	TGCCTGCTTC
301	TTTTTCTTCG	GCGGTGGCGC	GGACAACTG	GTCGTAAATT	TCGGCATAAA
351	GCATATCGTT	CGGGCCTTCA	AAAATCGTGA	AGGGGCGGAT	GTCGATAGCG
401	ATATTGCCGG	CGGTGTGTCC	GCGTTCAAAA	CCCTTCGCGC	CCAAGAGTTT
451	TTGCAACATT	TGCGCGGCGG	CGTAAGTGTA	TTCCGTGGCG	AGGGTTTTGA
501	CGATGTTTCG	CTCCATCAGT	TGATGGGCGA	CGGGTGCAAC	GGGCGAAACG
551	GAATGGCAGA	CGTAGCGGTA	AAGAATCTCG	GAAACCTGAT	GGCGGCGCCG
601	GATTTCGCGG	CGTTCGTAAT	CGACGAATCT	GATGTCGTTG	CGGACGTATC
651	GTTCCAGGTT	TTCAAGGGTG	TATTCATAA	TGCCGTGCGT	CATGCCGATC

1020

```

701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTGCAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GCGGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTGTCAGT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

m642.pep      10      20      30      40      50      60
ACRRICPLPAISAVQYIFADV VQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||:|||||
a642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADV VQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF

m642.pep      70      80      90      100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKL VVNFGIKHIV
|||||:|||||
a642          70      80      90      100     110     120
LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKL VVNFGIKHIV

m642.pep     130     140     150     160     170     180
RAFKNREGADVDSDIAGGVS AFKTLRTQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||:|||||
a642         130     140     150     160     170     180
RAFKNREGADVDSDIAGGVS AFKTLRAQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN

m642.pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADV SFQIFKDV FHNVRHADQLQAAAD
|||||:|||||
a642         190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADV SFQVFKGV FHNVRHADQLQAAAD

m642.pep     250     260     270     280     290     300
KDVLERAQTG SVALGEFHGGCRHFGIDAVDGVT DGAQAFGCEGFAADV CFGDEQQVDDF
|||||:|||||
a642         250     260     270     280     290     300
KDVLERAQTG SVALGEFHGGCRHFGIDAVDGVT DGAQAFGCEGFAADV CFGDEQQVDDF

m642.pep     310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGFGFGNTQT
|||||:|||||
a642         310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGFGFGNAXT

m642.pep     370     380     390     400
AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||:|||||
a642         370     380     390     400
AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP

```



370                      380                      390                      400

**g643.seq**

1	ATGGTGTTGC	CTTTGATGTT	GTTGGCGACA	ATCAGgTcgg	CTACGCTGAc
51	gttgtaGcGt	TTGGCaATGt	tGaaCAgggt	gtcgccTTCT	ACACGCGGT
101	GGATGCTGGC	ATGGagcGGG	GAGGTTTCGG	CTTCGCGCTG	GGCAGCTTTT
151	GCTACGCGCG	TTTCCAAACG	TGCCCGCGG	TtgcCGTCCG	CGCGAACGGT
201	ATGTTGCGGA	GATGAGGAAA	TGTTGTGTTC	GGCAACTGTG	TCAGGCGTGC
251	CGATGACGGC	GGagaTGGTT	TC TTCAGCCT	GCCGGCGCag	gTTGTTTCGG
301	GCAACAAGCT	GCATGAGTTC	GTCTGCCGCC	TGCATGTCTG	TTGGGGGGAt
351	GACCTGCGcG	aGTGtTGGCG	TTTGGGTTTC	agacgGCATG	GCAGTCTGTT
401	TTTcgGTTTG	a			

g643.pwp

1	MVLPLMLLAT	IRSATLTLXR	LAMLNRVSPS	TTRWMLAWSG	EVSASPSAAL
51	ATRVSKRARR	LPSAATVCCG	DEEMLCSATV	SGVPMTAEMV	SSACRRRLFR
101	ATSCMSSSAA	CMSFGGMTCA	SVAVVWSDGM	AVCFVS*	

**m643.seq**

1	ATGGTGTTGC	CTTTGATGTT	GTTGGCGACA	ATCAGGTCGG	CTACACTGAC
51	GTTGTAGCGT	TTGGCAATGT	TGAACAGGGT	GTGCGCTTCT	ACAACGCGGT
101	GGATGCTGGC	ATGGAGCCGG	GAGATTTCCG	TTTCGCGCGT	GGCAGCTTTT
151	GCTACGCGCG	TTTCCAAACG	TACCCGCGCT	CTTCGCTCGG	CGGCAGCGGT
201	ATGTTGCGGA	GATGCGGAAA	TTTTGTGTTC	GGCAACTGTG	TCAGGCGTGC
251	CGATGACGCG	GGAGATGGTT	TCCTCAGCCT	GTGGGCGCAG	GTTGTTTCGG
301	GCAACAAGCT	GCATGAGTTC	GTCTGCCGCC	TGCATGTCGT	TTTGGGGGAT
351	GATCTGCGCG	AGTGTTCGCG	TTTGGGTTTC	AGACGGCATG	GCGGTCTGTT
401	TTTCGGTTTG	A			

m643 . pep

```

1  MVLPLMLLAT  IRSATLTL*R  LAMLNRVSPS  TTRWMLAWSG  EISASPSAAL
51  ATRVSKRTRR  LPSAAAVCCG  DAEILCSATV  SGVPMTAEMV  SSACRRRLFR
101 ATSCMSSSAA  CMSFWGMICA  SVAVVUSDGM  AVCFSV*

```

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

m643/g643

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2067>:

1022

```

a643.seq
1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
351 GATCTGCGCG AGTGTTCGCG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTTCGGTTT A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
1   MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFSV*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMAVCFSVX					
a643	SVAVWVSDGMAVCFSVX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
1   ATGCCGCTCG AAAGGccgGC GGATTGTTCG CCGGTGCACT TTGTGGTAAA
51  GTTTAGAAAA TTAACCTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
201 ATTCcccccG ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCCTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGGTGTTC CAGCCTCTGC AAGagttcgg cggcgaagcG
451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAaggcgaaa gccgcggttt
501 gggcgTtacc gaaccgaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
551 agtcctgcta cgaatatacc gacgaacaAA CCATTTACGT caaCGCCGCG
601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgccgcaaa
651 agagcgcaaa aacGGcaaac tcgcaaaagt CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CCTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCCGGGGCG ACGCTGCCGG TTGCGCGCG TTCCAAAACA
851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGACAACTT GAACCGATAT GTCCGCAACG ATATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCCATCAG GTTCCGAAA
1001 TCCTTTACCG CTACGTCTGC CATTCGTTT CGcccgtcgC GCcgcTCCGC
1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCA CGGAATACAC
1101 TTAcgcCGCC GCGCAAATGT TGCAAAACT CTGGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 CGTCCGCGCC ACCGCCGAAG AAAAAAGAGC AGGCATTAAG TTGGACAAAA
1301 acccaaaCCCT Gctcgacgcc gtgCAaaccg atGTCcgctt tgCCGCCGTT
1351 GCCcgcGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GACGCCTGCG CCTGCAAAA AGTCTTCATC GGCAAAATCA

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1023

```
1451 TCGCCCGACT TTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
1551 ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

```
1 MPSEPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
51 QPSTMDTAAF LKHIESAFPR IFSDGIDLMR YLPEDKWLAL KOAGLLLPFL
101 DKKHGGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
151 QVAQGLDMIF KGESRRLGVT EPETSGAAIA REMQSCYEYT DEQTIYVNAA
201 KYWQGNQSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNFIRSRL QLIGMTHGIM
301 EYILDNLNRY VRNDIRFVDY ERREIQRRHQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGIK LDKNQTL LDA VQTDVRFVAV
451 ARDYALPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQEEHEDTTA
501 FLLNDIRKDI LDCRYCG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

```
1 ATGCCGCTCG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51 GTTTAGAAAA TCAACTCTAA ACTGTGCGAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCTTTC AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGCGCAG CAGTTTGAAA TCCAAGAAGT
351 CcTGCGGATT GCGGGGCGATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGCGCG GCTGGTGTTC CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAGTCGCGC AAGGTTTGGA GATGATTTTC AAAGCGGAGG GCGGCGGTTT
501 GGGTGTTACC GAACCCGAAA CCTCCGCGCG GCGATTGCA CGCGAAATGC
551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCCTG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCGCT
801 GATGAAACTC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
851 TCTTTATCCG CAGCCGCTCG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTTCCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCTGTTGC CCCGTCGCC
1051 CATCAGCTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGTGCG AAGGTTTTTG
1151 AACGCCGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGTGAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACACCAGTT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCTT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCCGCGCT ACACCTTGCC TGAAGACAT CGCAGCTTCC TGCAGGAACA
1401 CACCTGACG GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTGTCTTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
1551 GTAG
```

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

```
1 MPSEADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KOAGLLLPFL
101 DKKYGGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGEA
151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIA REMQSYEYI DGQTIYVNAA
201 KYWQGNQSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNFIRSRL QLIGMTHGIM
301 EYILENLERY VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTL LDA LQTDARFVAV
451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAKHEDTAA
501 FLLNDIRKDI LDCRYCG*
```

m644/g644 94.6% identity in 517 aa overlap

```
10 20 30 40 50 60
m644.pep MPSEADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
||||| :||||| :||||| :||||| :||||| :
g644 MPSEPADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
```

1024

	10	20	30	40	50	60
m644 . pep	70	80	90	100	110	120
g644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644 . pep	130	140	150	160	170	180
g644	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMIFKGEGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644 . pep	190	200	210	220	230	240
g644	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
	190	200	210	220	230	240
m644 . pep	250	260	270	280	290	300
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644 . pep	310	320	330	340	350	360
g644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
	310	320	330	340	350	360
m644 . pep	370	380	390	400	410	420
g644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644 . pep	430	440	450	460	470	480
g644	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLOEHTLT DACALQKVFI					
	430	440	450	460	470	480
m644 . pep	490	500	510			
g644	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644 . seq
1   ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGCGAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATGCCA TACCTGCCCC
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GGCGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAA TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCCGT
801 GATGAAACTC TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA

```

1025

```

851 TCTTTATCCG CAGCCGCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTTCGAGAG
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTTGAAG GCCCGAACGA TATGCTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCCGCGCC ACCGCGGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCTT GCTCGACCGC CTGCAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGCGCG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYET DGQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FRSRL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644/a644 97.3% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
a644	MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
a644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
a644	AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQAQGLEMIFKGGGGGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
a644	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
a644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
a644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK					

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
a644	TAEKEEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFVQAKHEDTAAFLNDIRKDILDCRYCGX					
a644	GKIIARLFVVFVQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGGTTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCACGC AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata cTGTCTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTACAG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGTCGCACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTTCGGCGAA
651 GTTTTGC GCG TGTGCTCGA CCAGAAGCGT GGTTCGGGCG AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GCGCACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGcggcgat ggcggcggcC TGGTCTTCGG
851 TTTCCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 . pep

```

1  MMMVLALGMS MPVSMMEQVS NTLNLCCKKS RMTCSRSSR SCPCATPIRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTL PLNGLTKVFT
101 ARRLGAVVI SEKSRRPSSA MLRVRGIGVA VMVRMSTLAR RRLSCSFRT
151 PKRCSSSIIN KPKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCTGTCTCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTGAATTT
501 GATGTCGTCC TGCACCAAGT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTTCGGCGAA
651 GTTTTGC GCG TGTGCTCGA CCAAAAGCGT GGTTCGGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GCGCACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCGGCGC TGGTCTTCGG

```

851 TTTCTTCGTA G

This corresponds to the amino acid sequence &lt;SEQ ID 2078; ORF 645&gt;:

m645.pep

```

1   MMMVLALGIS IPVSMMEQSN TLNRCCKKS RMTCSSSRSR SCPCATPMRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPPRLS SRNTASRTL PSLKGLTKVLT
101 ARRRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCA CCSTKSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMMEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGRSRVSSRSR	
g645	MMMVLALGMSMPVSMMEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPIRA	SGRSRVSSRSR	
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPRLSS	RNTASRTLPSL	KGLTKVLTARRRL	GAVVISEKSR	SPSNA	
g645	IFSIVSTSLCRKNTCPPRLSS	RNTASRTLPSL	NGLTKVFTARRRL	GAVVISEKSR	SPSSA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLAR	RRRLSCSF	XRTPKRCSSSIIT	KPKFLNLMSS	CTSLCVPITI	
g645	MLRVRGIGVAVMVRISTLAR	RRRLSCSF	CRTPKRCSSSIIT	KPKFLNLMSS	CTNLCVPITI	
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLK	RERLATFTG	KSARKSAKFCAC	CTKSVVGAST	ATCLPPIT	
g645	STVPSAMPSSVALVALLLK	RERLATFTG	KSARKSAKFCAC	CTRSVVGAST	ATCLPPIT	
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPH	TRRSIGFACVK	SLITAAMAAW	SSVSSX		
g645	ATNAARRATSVLPKPTSPH	TRRSIGFACVK	SLITAAMAAW	SSVSSX		
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq

```

1   ATGATGATGG TGTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAGTT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGCGCAAA
651 ATTTTGC GCG TGCTGCTCGA CCAGAAGCGT GGTCGGTGCG AGTACGGCAA
701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GGCGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCTGCC TGGTCTTCGG
851 TTTCTTCGTA G

```

This corresponds to the amino acid sequence &lt;SEQ ID 2080; ORF 645.a&gt;:

a645.pep

```

1   MMMVLALGMS IPVSMMEQSN TLNRCCKKS RMTCSSSRSR SCPCATPMRA

```

1028

```

51  SGSRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTL P SLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

m645/a645 96.9% identity in 286 aa overlap

      10      20      30      40      50      60
m645.pep MMMVLALGISIPVSMMEQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      MMMVLALGMSIPVSMMEQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
          10      20      30      40      50      60

      70      80      90      100     110     120
m645.pep IFSIVSTSLCRKNTCPPLRSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
          :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      MFSMVSTSLCRKNTCPPLRSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
          70      80      90      100     110     120

      130     140     150     160     170     180
m645.pep ILKVRGIGVAVMVRISTLARRRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      ILKVRGIGVAVMVRMSTLARRRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
          130     140     150     160     170     180

      190     200     210     220     230     240
m645.pep STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
          190     200     210     220     230     240

      250     260     270     280
m645.pep ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645      ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
          250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTGCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51  GFKGTVGQTE RGTVAADTV FRQIVGVDD TDAERTAVHS RGTRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```



	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	:     :     :     :     :     :     :     :     :     :					
g647	MQRLAADGIQIFFVGVSDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVAVADTVFRQIISIVNHADAERTA AHSRGTRGFYRISLIIX					
	:     :     :     :     :     :     :     :					
g647	RGTVAVADTVFRQIVGVDDTDAERTA VHSRGTRGFYRISLIIX					
	70	80	90	100		

```
a647.seq
1  GTGCAAAGGC  TCGTTACACA  CAGCGTCCAA  GTCTTTTTTG  TAGGTGTCTGA
51  TGGGCAGTTT  GCCTTGCCAA  TAAACGGTTT  GGTAAAGAG  CAGTGCACGCA
101 CCGTATTCTT  TGGCAAGGTT  TCCGCAATGCT  TTGAGCAGGT  AATACTGTAT
151 GGCTTCAAAG  GTACGGTGGG  TCAGACCGAG  CGCGGAGCCG  TCGCTGTAGC
201 GGACACCGTT  TTTTCGCCAA  TAATACGCAT  AGTTGATCAC  GCCGATACCG
251 AGCGAACGGC  GGCCCATAGT  GGAGGTACGC  GCGGCTTCTA  CCGGATATCC
301 CTGATAATCT  AA
```

a647.pap  
1 VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY  
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS  
101 LII\*

	10	20	30	40	50	60
m647.pep	MQRLAADGIQI	FFVSV	DGQFALR	INGLVKERART	VFFGKVCRCFEQ	VILYGFKGTVGQTE
a647	VQRLVTHSVQV	FFVGV	DGQFALR	INGLVKERART	VFFGKVCRCFEQ	VILYGFKGTVGQTE
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVA	VADTVFRQII	SIVNHADAERTAAH	SRGTRGFYRISLIIX		
a647	RGAVA	VADTVFRQIIR	IVDHADTERTAASG	GTRGFYRISLIIX		
	70	80	90	100		

```
g948.seq
1  ATGAACAGGC  GCAACGCGCG  GATCGAACGG  GCTGTGCGTA  TTGCAGTGTAT
51  CGACGTTTGT  AATGTAGATG  GCCCGGTGCC  CGGCACGCTC  TGTGCATCAGC
101  TTGGAAACA  GGTGCGCAGC  CGGAATGATA  CGTGTGCGTA  TGTTCCGGTC
151  TTGCTCGTAT  TTCGTATAGA  GCCGCTCAA  TTCGTCTTGG  TCGGCAAAAA
201  ACGCTTCGTA  CAACCCCGAA  ACCTCGTTGG  CGGAAAAACG  CGTAATGTGTG
251  CGCCCTTAA  TACGGCGGGT  GTACAGCAG  CGGTTGATT  GCACGCATCA
301  ATCAAGCTGG  CGGATACGGT  TGCTTCCAC  GCCCGGTTG  TTTTCAACA
351  CCAGCAGGCT  TTCGGCTTCA  ATATGCCACA  AGGGGTAGAA  CAAAGTTGCC
401  GCGCGCGCG  GCACGCCAAC  TTGCGCAATA  GATTTGACC  CCGCTTGAAA
451  CATCTTAAAG  AAGGGAATGC  AGCCGGATCA  CCGGGCTTCA  CGCCGCCGGA
501  TTTCGCTGTC  CAGCCCGCGG  ATACGTCGG  CATTGATGCC  GATGCCCGCG
551  CGTTGGGAAA  CGTATTTCAC  AATCGCGCTG  GTAGTGGCAT  TGATGGAATC
601  CAAACTATCG  TCGCATTCAA  TCAGCACACA  GCTTGA
```

g648 . pep

1 MNRNRNARIER AVRIAVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV  
51 LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVIDLHAI  
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV E QGCRAAAHAT LRTFRDRLK  
151 HLKEGNAAG PGFTAPDFAV QPADTSGIDA DARALGNVHF NRAGSGIDGI  
201 QTIVAFNQHT A\*

**m648.seq**

m648 . pep

m648/g648 91.5% identity in 211 aa overlap

a648.seq

1	ATGAACAGGC	GCAACGCGCG	GATCGAACGG	GCTGTGCGTA	TTGCAGTGTAT
51	CGACGTTTTG	AATGTAGATG	CGCCGGGTTT	CGGCACGCTC	CTGCATCAGC
101	TGTGAAAAAC	GGTCGGCAGC	CGGAATGATG	CGCTTGCCTG	TATCAGGGTC
151	TTGCTCGTAT	TTCTGTATAG	ACCGCTCAAA	TTCTGCTTGG	TCGGCAAAAA
201	ACGCTTCGTA	CAATCCCGGA	GCTTCGTTGG	GCAGAAAACAG	CGTAATGTGT
251	CCGCCCTTAA	TCAGGCGGGT	GTACAGCAGG	CGGTTGATTT	GCACGCCGTA
301	ATCAAGCTCA	CGGATACGGT	TGCTTCCAC	GCCCCGGTTG	TTTTTCAACA
351	CCAGCAGGCT	TTCCGGCTTC	ATATGCCACA	AGGGGTAGAA	CAAGGTTGCC
401	GCGCCGCCCG	GACGCCACCC	ATCCGAACAG	GATTTGACTG	CCGCCTGAAA
451	CATTTTAAAG	AAGGGAATGC	AGCCGGTATG	CCGTGCTTCG	CCGCCCCGGA

1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA  
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC  
 601 CAGGCTGTCTG TCGCATTCGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep  
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV  
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV  
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCRLK  
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI  
 201 QAVVAFDQYA A\*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHTAVVFQHQQA					
a648	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPQGV E QGCRAAAHAAALRTGFDRRLKHFEKNAAGMPRFAAPDFAVQTADTSGIDA					
a648	FGFDMPQGV E QGCRAAAHATLRTGFDCRLKHFEKNAAGMPCFAAPDFAVQSADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAAGSGIDGIQTIVAFNQHTAX					
a648	DARTLGNVFHNRAAGSGVDGIQAVVAFDQYAA					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq  
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGA CTGGTAT CAACA ACTGC  
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCAGCA  
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC  
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA  
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA  
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG  
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep  
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECKRYLER  
 51 RAAWYRSQGN VQELRENKKA RKAFTLPYA EQKIQCRAAY EAFDDFDGGR  
 101 FRR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq  
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGA CTGGTAT CGACA ACTGC  
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA  
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC  
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA  
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA  
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT  
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649           MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
g649           VQELRENKKARKAFRTLPYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTGGAACGC
151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2098; ORF 649.a&gt;:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649           MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
a649           VQELRENKKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCGCAG CTATTTGAC AGGGTCGTCA ACCGAGACCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGAAAA AAACaccgGT TTACGacggc aggcacGacg TTtacgcaGc
501 taccgatgcc gcacTCAACT AtctGcAATA TCTCTatggA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCGTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACC CCAATCTT TCGGCATGAA TATCAGCGAC

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1033

```

751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTC AAC GTCCCGCGt tcatCCCCAA AAaCaacgc
901 aaacTGCTGC TTCCTGTGCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCTTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCCggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccc
1251 cgcaCAGACA gcggacatta ccgtcgcacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatccctc tgtccgcaTt accgaaccg ccctTGCAGC
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

**g650 . pep**

```

1 MSKLKTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGRMGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDYRSN
401 MPAGTVNVSI ARIQFAAAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

**m650 . seq**

```

1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCGAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCCG
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCGGCG
551 ACTGGCCGCT TGCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGCA
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTTAAACCC CGCATTC AAC GTCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGC TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG . AAC CCGATCCCTT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

**m650 . pep**

```

1 MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGRMGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

```

**m650/g650** 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLKTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGFRMGEVNPPELVRRHESKFIASHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
g650	LRQGFRMGEVNPPELVRRHESKFIASRSYFDRVVNRSRPYMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGSGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGSGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEVNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
g650	LFGDWPLAFAAYNWGEVNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSFGMNIISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFGMNIISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDTPYRSNMPAGTVNVGRIARIPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIDIDNTPDTPYRSNMPAGTVNVSIARIQAAAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRXTXTRSPCPYCRTCPCDSRSATSNRKTDHRAVX					
g650	ADITVAPLPQETVRTGTRSPCPHYRTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

```

a650.seq
1  ATGTCCAAAC  TCAAAACCAT  CGCCCTGACC  GCGTCAGGTC  TGTCCGTTTG
51  TCCGGGTTTC  CTATACGCCC  AAAACACCTC  ATCACACCAA  ATCGGTTTGG
101 CGATTATGCG  CTTAAACTCT  TCAATACTCG  ACCTGCCACC  GACAAAACAA
151 TATTTCCAAT  CCGGCAGCCT  GTGGAGCGAG  CTGCGCCAAG  GCTTCCGGAT
201 GGGCGAAGTC  AATCCCGAAC  TGGTACGCCG  CCACGAAAGC  AAATTCATCG
251 CAAGCCACAG  CTATTCAAC  AGGGTCATCA  ACCGGAGTAG  ACCCTATATG
301 TACCATATCG  CCAACGAAGT  CAAAAACGC  AATATGCCCG  CCGAAGCCGC
351 CCTGCTTCCC  TTCATCGAAA  GCGCGTTCGT  CACCAAAGCC  AAATCACACG
401 TCGGCGCATC  GGGCCTGTGG  CAGTTCATGC  CCGCTACCGG  CAGGCATTAC
451 GGCCTGGAAA  AAACACCGGT  TTACGACGGC  AGGCACGACA  TTTACGCCGC
501 CACCGATGCC  GCACTCAACT  ATCTGCAATA  CCTCTATGGA  CTGTTCCGGC
551 ACTGGCCGCT  CGCCTTTGCC  GCCTACAAC  T  GGGGTGAAGG  CAACGTCGGA
601 CGCGCCATCA  ACCGCGCCCG  CGCCCAAGGG  CTCGAACCGA  CCTACGAAAA
651 CCTGCGTATG  CCCAACGAAA  CGCGCAACTA  TGTTCCCAAG  CTGCTCGCCG
701 TGCGCAACAT  CATTGCCGCC  CCCCATTCTT  TCGGCATGAA  TATCAGCGAC
751 ATAGACAACA  AACCGTATTT  TCAGGCAGTC  GAACCGGACC  GTCCGCTCGA
801 CAACGAAGCC  ATCGCCCGGC  TTGCCGGCAT  CACGCAAAGC  GAGCTGCTCG
851 CCTAAACCC  CGCATCAAC  GTCCCGCGT  TCATCCCCAA  AAGCAAACGC

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1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAACCAG CTGTGCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCGTATT GCCGAACCTG CCCTTGCAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

a650.pep

```

1  MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGFMRGEV NPELVRRHES KFIASHSYFN RVINRSRPFY
101 YHIANEVKKR NMPAEAAALL FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/a650 99.1% identity in 465 aa overlap

	10	20	30	40	50	60
m650.pep	MSKLKTIALTASGLSVCPGF LYAQNTSSHQ IGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
a650	MSKLKTIALTASGLSVCPGF LYAQNTSSHQ IGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m650.pep	LRQGFMRGEVNPELVRRHESKFIASHSYFN RVINRSRPFYMYHIANEVKKRNMPAEAAALLP					
a650	LRQGFMRGEVNPELVRRHESKFIASHSYFN RVINRSRPFYMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m650.pep	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
a650	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m650.pep	LFGDWPLAFAAYNWEGENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
a650	LFGDWPLAFAAYNWEGENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m650.pep	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR					
a650	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m650.pep	KLLLPVASVQTFQSNYLNAAPDSLFSWEVYT PAAKTSLSDISTATGMSIADIKRLNNLNG					
a650	KLLLPVASVQTFQSNYLNAAPDSLFSWEVYT PAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m650.pep	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT					
a650	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT					

1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRXTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
a650	ADITVAPLPQKTVRXTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCGGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATACTTGGA GGCTTGTTA
551 ACGAATTCCC GATTATTTC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATTCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGc cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAccgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAaaaccgG TTCTTTGAGc
901 cgTTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCgcctACT ACCCCGGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
201 EGWKLLEFKL GKVVQLVGDD LFTVNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEELAE AAYYPGKAFF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAAGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGA GGCTTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGTAGAG TTCAATTGGT
651 TGCGGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAa CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```



1037

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC  
 151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW  
 201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT  
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS  
 301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK\*

m652/g652 98.2% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
g652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
g652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
g652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPPIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
g652	GLVNEFPPIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
g652	LLVKVNQIGTLSETLKAVDLAKCNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
g652	RSDRMAKYNQLLRIEEELAEAAAYPGKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

a652.seq

1	ATGATCGAAT	TGGACGGTAC	TGAAAACAAA	GGCAATTTGG	GTGCGAATGC
51	GACTTTGGCG	GTTTCTATGG	CGGTTGCACG	CGCCGCTGCC	GAAGACTCAG
101	GCCTGCCGCT	TTACCGCTAC	TTGGGCGGCG	CAGGCCCGAT	GTCCCTGCCC
151	GTACCGATGA	TGAACGTCAT	CAACGGCGGC	GAACACGCCA	ACAACAGCCT
201	GAACATCCAA	GAGTTTATGA	TTATGCCCGT	CGGCGCAAAA	TCTTTCCGCG
251	AAGCGTTGCG	CTGCGGTGCG	GAAATTTTCC	ACGCCTTGAA	AAAACGTGTC
301	GACAGCAAAG	GCTTCCCGAC	CACAGTCGGC	GACGAAGGCG	GTTTCGCCCC
351	CAACCTGAAC	AGCCACAAAG	AAGCCCTGCA	ACTGATGGTC	GAGGCGACCG
401	AAGCCGCCGG	CTACAAAGCG	GGCGAAGACG	TATTATTCGC	ATTGGACTGC
451	GCGTCCAGCG	AGTTCTACAA	AGACGGCAAA	TACCACTTGG	AAGCCGAAGG
501	CCGCTCCTAC	ACCAACGCGG	AATTTGCCGA	ATATCTGGAA	GGCCTGGTCA
551	ACGAGTTCCC	CATCATCTCC	ATCGAAGACG	GGATGGATGA	AAACGACTGG
601	GAAGGCTGGA	AACTGCTGAC	CGAAAAACTG	GGCGGCAAG	TCCAACCTCGT
651	TGGCGACGAC	CTCTTCGTTA	CCAACCCGAA	AATCCTTGCC	GAAGGCATTG
701	AAAAAGGCGT	GGCAAACGCA	CTATTGGTCA	AAGTCAACCA	AATCGGTACT
751	TTGAGTGAAA	CCCTGAAAGC	CGTCGACTTA	GCCAAACGCA	ACCGCTACGC
801	CAGCGTAATG	AGCCACCGCT	CCGGCGAAAC	CGAAGACAGC	ACCATGCGCG
851	ACTTGGCAGT	CGCCACCAAC	TGTATGCAGA	TCAAAACCGG	TTCTTTGAGC
901	CGTTCCGACC	GCATGGCGAA	ATACAACCAA	CTGCTGCGTA	TCGAGGAAGA
951	ATTGGCGGAA	GCCGCCGACT	ACCCAGCAA	AGCCGCATTG	TACCAACTGG
1001	GCAAATAA				

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

a652.pep

1	MIELDGTENK	GNLGNATLA	VSMVARAAA	EDSGLPLYRY	LGGAGPMSLP
51	VPMNVINGG	EHANNSLNIQ	EFMIMPVGAK	SFREALRCGA	EIFHALKKLC
101	DSKGFPTTVG	DEGGFAPNLN	SHKEALQLMV	EATEAAGYKA	GEDVLFALDC

1038

151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW  
 201 EGWKLLETKL GGVQLVGGD LFVTNPKILA EGIEKGVANA LLVKVNQIGT  
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS  
 301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK\*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
a652	EHANNLSNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTLSETLKAVDLAKRNRYASVMHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNQIGTLSETLKAVDLAKRNRYASVMHRSGETEDSTIADLAVATNCMQIKTGSLS*					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
a652	RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCCGCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGCCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTCCGCGACG GCGACAAATC CCGCTATTCC GGCAAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTGGG TGCGAATGCG ACTTGGCGG TCTCTATGGC
351 GGTTCACGCG GCCGTCGCC AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGCGCAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGTAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCCGCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGCGAAAT ACCACTTGA AGCCGAAGGC CGTCCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTCGCG ATTATTTCGA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GGCGACGACT TGTTCGTAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGATCTGG CAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGTCGCTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCCCAGCAA GCCGATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

## g652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEF AE YLEGLVNEFP IISIEDGMDE NDWEGWKL LT
301 EKLGGKQVLV GDDLFTNPK ILAEGIEKGV ANALLVKVNO IGTLS ETLKA
351 VDLAKCNRYA SVMSHRSGE T EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

## m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
201 GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGAATCGAAT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGTGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGCGGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGCAAAGG CTCCCGACC
601 ACAGTCGGCG ACGAAGCGCG TTTCGCCGCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGGC TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAA T ACCACTTGG AAGCGAAGG CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGCAGACT TGTTCGTAA C
951 CAATCCAAAA ATCTTGGCGG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CCGCGAAEAG GAAGACAGCA CCATTGCCGA CTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCAGCAAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

## m652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEF AE YLEGLVNEFP IISIEDGMDE NDWEGWKL LT
301 EKLGGKQVLV GDDLFTNPK ILAEGIEKGV ANALLVKVNO IGTLS ETLKA
351 VDLAKRNRYA SVMSHRSGE T EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGD KSRYS					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGD KSRYS					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANNSLNIQEFMIMPV GAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVI NGGEHANNSLNIQEFMIMPV GAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKL	CDSKGFPTTV	GVGDEGGFAP	NLNSHKEAL	QLMVEATEA	AAGYKAGEDV
g652-1	CGAEIFHALKKL	CDSKGFPTTV	GVGDEGGFAP	NLNSHKEAL	QLMVEAAEA	AAGYKAGEDV
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYK	DGKYHLEA	EGRSYTN	AEFAEYLE	GLVNEFP	IIISIEDG
g652-1	LDCASSEFYK	DGKYHLEA	EGRSYTN	AEFAEYLE	GLVNEFP	IIISIEDG
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQ	LVGDDLF	VTNPKIL	AEIEKGV	ANALLVK	VNQIGT
g652-1	EKLGGKVQ	LVGDDLF	VTNPKIL	AEIEKGV	ANALLVK	VNQIGT
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSG	ETEDSTI	ADLAVAT	NCMQIKT	GSLSRSD	RMAYNQ
g652-1	SVMSHRSG	ETEDSTI	ADLAVAT	NCMQIKT	GSLSRSD	RMAYNQ
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

## a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAGGGCGG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGACACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCCTACT
401 TGGGCGGGCG AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGCACAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCGC ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGTGGGAA ACTGCTGACC
901 GAAAAACTGG GCGGCAAAAT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

## a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGAANA TLAVSMAVAR AAAEDSGLPL YRYLGAGGPM SLPVPMNVI
151 NGGEHANNLS NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLF A LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKVQLV GDDLFVTNPK ILAEGIEKGV ANALLVKV NQ IGTLSLTKA
351 VDLAKRNRYA SVMSHRSGE EDSTIADLAV ATNCMQIKT G SLSRSDRMAK
401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESQVGMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESQVGMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      70      80      90      100     110     120
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR
              70      80      90      100     110     120

m652-1      130     140     150     160     170     180
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      190     200     210     220     230     240
a652-1      CGAEIFHALKKLCDKSGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      250     260     270     280     290     300
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPFIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      310     320     330     340     350     360
a652-1      EKLGGVQLVGDDLFTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      370     380     390     400     410     420
a652-1      SVMSHRSGETEDSTIADLAVATNCMIKTGSLRSRDRMAKYNQLLRIEEEELAEADYPSK
              370     380     390     400     410     420

m652-1      429
a652-1      AAFYQLGKX
              |||||
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

## g653.seq

```

1   ATGGCGGcg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTT TGTtgacggT GATGTGCGCt ttgccccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaactGTCG TTTCGGTGCG GCCGGAaag atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgGCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGcAGG CTTGGAAGA TGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTgG ttACgaaGtC GCAGAatggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

## g653.pep

```

1   MAAEPMRPE VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

## m653.seq

```

1   ATGGCAGCGG AGCCGATGCG GATGCCGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTT TGTtgacggT GATGTGCGCt TTGCCCCAAG
101 CGGCTTCGGC GGCTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```

151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTGGG GATATTCGCC GCCGGAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
g653           MAAEPMRMPEVTYGFSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
g653           MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
              70      80      90      100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX
              |||||
g653           SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATSPAX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGGCGGCGG AACCGATGCG GATGCCGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCTGG ATGGCGTTT TGTTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

              10      20      30      40      50      60
m653.pep      MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
a653           MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m653.pep      MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
a653           MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              70      80      90      100     110     120

              130     140     150     160
m653.pep      SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX
              |||||
a653           SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX

```

130                      140                      150                      160

```
g656.seq
1  ATGCCGCGTT TCTCCGTTTC GATTTCTTCG ATGATTTCCTA TC GCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TG Ccggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGC ctTCGAGCTT GGAAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTTCGG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTCTG
301 TTGGCAAGGT CTTCCGCGGG GGTTTTGGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCTGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAT CGTAG
```

g656.pep  
1 MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM  
51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIITCSAI SLASLNKSCS  
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTS ISGEEPTMWK SPKS\*

```
m656.seq
1  ATGCCGCGTT TGCTCGGTTT GACTTCTTCG ATGATTTCCT TGCGCGGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGCTCT TTCAGACGGC CTTCTGACGT GGAACGATGT
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTGCG TAACTTTGAC
201 TTCGCCGGTT TTAATGATGC GGCCGACGTC GTTGCGTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCT
301 TTGGCAAGGT CTTCCGCGGG GGTTTTCCCG CGCAGGCGCG TGCCGGCGAT
351 GGGCGGACG ATAACGTCGT TCGGTTCCGG TCGGACGAGG ATTTCTGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAT CGTAG
```

```
m656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPFS FRRPSTLETM
51  CITWEYFSIT ILSVTILTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLSRRRTR ISGEEPTMWK SPKS*
```

Homology with a predicted ORF from *N. gonorrhoeae*

**m656/g656** 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMIS	MARTLGAPESV	PAGKVAARMS	MLVMPSEFR	RPSTLETMCIT	WEYFSIT
	:		:		:	
g656	MPRFSGSISSMIS	IARTFGAPESV	PAGKVAARMS	ILVTPSFQK	PSTLETMCIT	WEYFSIT
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLL	MRPTSLRPKS	INMTCSAISL	ASLNKSCSL	ARSSAGVLP	RRRVFAMGR
		:				
g656	ILSVTLTSPVLL	MRPTSLRPKS	ISITCSAISL	ASLNKSCSL	ARSSAGVLP	RRRVFAMGR
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRSRRTRIS	GEEPTMWKSP	KPSX			
	:					
g656	MTSSRSRRTRIS	GEEPTMWKSP	KPSX			
	130	140				

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACTTTGAC
201 TTCGCCGTTT TTAATGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTGGCGGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTGCGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP K SINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPs	FRRPSTLETMCITWEYFSIT			
a656.	MPRLLGSTSSMISMARTLGA	PESVPAGKVAARMSMLVMPs	FRRPSTLETMCITWEYFSIT			
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
a656	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
a656	ILSVTLTSPVLLMRPTSLRP	KSINMTCSAISLASLNKSCS	LARSSAGVLP	RRRVPAMGRT		
	70	80	90	100	110	120
m656.pep	ITSLRSRRTRISGEEPTMWK	SPKSX				
a656	MTSSRSRRTRISGEEPTMWK	SPKSX				
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTCGCGGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGGCGGTta cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTACAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGT GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcC ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCGta
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGAGCA CAGTTCCAA CAGCAGGTAC GCATTATGTG CAACctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTTGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAAC CGCAGAGAAA
1051 GGTCGGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:



1045

g657.pep

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GVDGKGQIRV	KTLDLKAFF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQARQTAQR	LADELDYVGV

1046

251 LAVEMFVVG D THELLVNETA PRTHNSGHHT IDACAADQFQ QQVRIMCNLP  
 301 PADTKLLSP C MANILGDVW QEDGGE PDWL PLQSRPNAHL HLYGKKTAQK  
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq  
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG  
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA  
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC  
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT  
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCGGATG  
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTAG CGGCGATTGT  
 301 GTGGCGATTG CACAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC  
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA  
 401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG  
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACTCAA  
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG  
 551 TGGATTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC  
 601 AACGTGCAAA CTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT  
 651 GGCTTATTCC ATCGTCCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG  
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTGCGCGTA  
 751 TTGGCGGTAG AAATGTTTGT TGTGCGTGAC ACGCATGAAT TGGTCGTCAA  
 801 CGAAATCGCC CCGCGCCCGC ACAATCCGG ACACCATACG ATAGATGCCT  
 851 GCGCAGCAGA CCAGTTCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG  
 901 CCTGCCGATA CCAAATTACT GAGTTCTTGC TGTATGGCAA ATATTTTGGG  
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA  
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA  
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTTA ACCACCGATT CGGACACCGC  
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep  
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAPAAEFA  
 51 DRHLCAPFND QAALDELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC  
 101 VAIAQNRIQE KAWIRKAGLO TAPYQVCKA EDITEASAQF LPGILKTATL  
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND  
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADEL DYGV  
 251 LAVEMFVVG D THELVVNEIA PRPHNSGHHT IDACAADQFQ QQVRIMCNLP  
 301 PADTKLLSS C MANILGDVW QEDGGE PDWL PLQSHPNAL HLYGKKTAHK  
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAM	LGILGGGQLGR	MFTVAAKTM	GYKVTVLDP	DPDPAPAAE	FADRHLCA
	10	20	30	40	50	60
g657	MNTPPILPPAM	LGILGGGQLGR	MFAVAAKTM	GYKVTVLDP	DPNAPAAE	FADRHLCA
	70	80	90	100	110	120
m657.pep	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGD	CVIAIAQNRI	QEKAWIRKAG
	70	80	90	100	110	120
g657	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGD	CVSIAQNRI	QEKAWIRKAG
	130	140	150	160	170	180
m657.pep	TAPYQVCKA	EDITEASAQFL	PGILKTATL	GYDGKGQIR	VKTLDLKA	FAEHGGVDC
	130	140	150	160	170	180
g657	TAPYQAVCKA	EDITEASAQFL	PGILKTATL	GYDGKGQIR	VKTLDLKA	FAEHGGVDC

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
	:     :     :     :     :     :					
g657	EKMVDLRGEISVIVCRLNNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
	:     :     :     :     :     :					
g657	LADEL DYVGV LAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAHKGRKMGHFTVL					
	:     :     :     :     :     :					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAQKGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSLX					
	:     :     :     :     :					
g657	TTDSDTAFQEAKKLHQSLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAATGT TTACTGTTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTACAGGA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCAGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTGG GAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCGC ACAATTCCGG CCACCATACC GTCGACGCTT
851 GCGCGGCAGA CCAATTCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCCGCGCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTAL EELAKK AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESI QF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQQARQMAQR LADELNYVGV
251 LAVEMFVVGDTHEL VVNEIAPRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWF PLQSRPDAHL HLYGKKTAHK
351 GRKMGHFTIL STDSDTAFQE AKKLHQSL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPAPAAEFADRHLCAFPND					

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|||||
a657      MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCPFDN
           10      20      30      40      50      60

           70      80      90      100     110     120
m657.pep  QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
           |||:|||||
a657      QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
           70      80      90      100     110     120

           130     140     150     160     170     180
m657.pep  TAPYQVVCKAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDLKAFAEHGGVDCVL
           |||:|||||
a657      TAPYQAICKAEDITEESIQLFLPGILKTATLGYDGKGQIRVKTVDLKAFAEHRGVDCVL
           130     140     150     160     170     180

           190     200     210     220     230     240
m657.pep  EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR
           |||:|||||
a657      EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQQARQMAQR
           190     200     210     220     230     240

           250     260     270     280     290     300
m657.pep  LADEL DYVGLAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
           |||:|||||
a657      LADEL NYVGLAVEMFVVGDTHEL VVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP
           250     260     270     280     290     300

           310     320     330     340     350     360
m657.pep  PADTKLLSSCCMANILGDVWQEDGGE PDWLP LQSHPN AHLHL YGKKT AHKGR KMGHFTVL
           |||:|||||
a657      PADTKLLSSCCMANILGDVWQEDGGE PDWFP LQSRPD AHLHL YGKKT AHKGR KMGHFTIL
           310     320     330     340     350     360

           370     379
m657.pep  TTDSDTAFQEAKKLHQSLX
           :|||||
a657      STDSDTAFQEAKKLHQSLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2135>:

```

g658.seq
1  ATGGTGGCCG GAATTGTGCG TGC GCGGGGCG GGTTCATTG ACGAGCAATT
51  CATGTGTGTC GCCGACAACA AACATTCTA CCGCCAAtac GCCGACATAA
101 TCCAATTTCGT CCGCCAagcG TTGCGCCGTC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGCCGCGcgg gGACGATGga atAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCGGGG TCGAAGGTTT GCACGTTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAAT CTCGCCGCGC AAGTCCACCA TTTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCGTCCA
351 ACGTTTTGAC GCGGATTTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGCACAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTTGCAAAACC GCCTGATACG GCGCGGTTT CAAGCCTGCT TTGCGTATCC
501 ACGCTTTTTT CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gtTTTCAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCGGTC GTCAAACGGC GCGCACAAAT GGCGGTGCGC AAATTCGGCC
701 GCCGGCGCAT TCGGGTCGGG ATCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTAGCGGCA ACGGCAACA TTctgcctAA

```

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

```

g658.pep
1  MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLL
51  VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

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1049

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101 NAIHAAVFGK RGEFFVQRFD ADLTFVAVAQ RSRFQDAGQK LRACFSNVFG
151 LANRLIRRLG QACFAYPRFF LNAVLCNGHA VAAGGNVGM L CQRAHRVGID
201 VFKEGRNRRR FCQFVQRGPV VKRRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHS A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```
m658.seq
1  ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTTCTGTTG ACGACCAATT
51  CATGCGTGTC ACCGACAACA AACATTTTCTA CCGCCAAATAC GCCGACATAA
101 TCCAATTCTGT CCGCCAAGCG TTGCGCCATC TCGCCGCGCT GCTCTGTCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGATT GCACGTTGTC ATTGTTCAAA
251 CGGCATACGA TTACGGAAAT TTCATTGCGC AAATCCACCA TTTTTTCCAA
301 AACGCAATCC ACGCCGCGGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTTAC GCGGATTTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTTG CAATCCCGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGTCGAA TCGCCACACA ATGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGCGATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCAAAG
651 CAGCTTGCTC GTTAAACGCG GCGCACAAT GGCGGTCGGC AAATTCTGCT
701 GCGCGCGCGT CCGGATCGGG TCGAGAACG GTTACTTTGT AGCCCATGTT
751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA
```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```
m658.pep
1      MVSGIVRARG  DFVDDQFMRV  TDNKHFYRQY  ADIIQFVRQA  LRHLPLRLLLH
51     VGTQSRGDDG  ISQDAVEFDV  FGRVESLHV  IVQTAYDYGN  FTAQIHFFQ
101    NAIHAAVFGK  RGFEFIQCFY  ADLTFAVVAQ  RSRFQDAGQK  LRACFSDVFS
151    LTNHLIRRLGL  QSRFAYPCLF  LNAVLCNRHT  IAARGNIGMF  CQKAHRIGID
201    VFKFSGHRRA  FCQFVQSSLV  VKRRAQMAVG  KFCCRRVRIG  VENGYFVAHG
251    FGGNGKHS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m658/g658** 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQ	FMRVTDNKHFYRQYADII	QFVRQALRHLPRLL	LLHVGTQSRGDDG		
g658	:	:	:			
	10	20	30	40	50	60
m658.pep						
g658	MVAGIVRARGGFIDEQ	FMCVADNKHFYRQYADII	QFVRQALRRLPRLL	LLHVGTQPRGDDG		
	10	20	30	40	50	60
m658.pep						
g658	ISQDAVFVDVFGRVESL	HVVIVQTAYDYGNF	TAQIIHFFQNAIHA	AAVFGKRGFEFI	QCIFY	
	70	80	90	100	110	120
m658.pep						
g658	ISQDAVFVDVFGGVEGL	HVFIVQTAYDHGNL	AAQVHHFFQNAIHA	AAVFGKRGFEFV	QRFD	
	70	80	90	100	110	120
m658.pep						
g658	ADLTFAVVAQRSRFQD	AGQKLRAFCSDFVSL	TNHLIRRLQSRFAY	PCFLNAVLCNRHT		
	130	140	150	160	170	180
m658.pep						
g658	ADLTFAVVAQRSRFQD	AGQKLRAFCSNVFGL	ANRLIRRLQACFAY	PRFFLNAVLCNGHA		
	130	140	150	160	170	180
m658.pep						
g658	IAARGNIGMFCQKAHR	IGIDVFKFSGHRR	AFCQFVQSSLVVK	RRAQMAVGKFC	CRRVRIG	
	190	200	210	220	230	240
m658.pep						
g658	VAAGGNVGMLCQRAHR	VGIDVFKFGRNRR	AFCQFVQRGPVVK	RRAQMAVGKERRR	IRVG	
	190	200	210	220	230	240
m658.pep						
g658	VENGYFVAHGFGGNG	KHSAX				
	250	260				

1050

```

          :|||||:|||||
g658      IENGYFVAHGFSNGKHSAX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
  1  ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
 51  CATGCGTGTC GCCGACAACA AACATTCTA CCGCCAATAC GCCGACGTAG
101  TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
151  GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
201  CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTCAGA
251  CGGCATACGA TAACGGAAAT TTCGCGCGCG AAGTCCACCA TTTTTCCAA
301  AACGCAATCC ACGCCGCGGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA
351  CCGTTTTGAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTCGCGTT
401  TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
451  TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC
501  ATGCCTTTTC CTGAATGCGG TTTTGCGCGA TGGCAACGCA GTCGCGCGTG
551  GGGGAAACAT TGGTATGTTT GGCGAGAAAA CGCATCGCAT CGGCATTGAC
601  GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG
651  CGGTTTGGTT GTCAAACGGC GCACACAAAT GGCGGTGCGC AAATTCGCGT
701  GCCGGCGCAT TCGGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
751  TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
  1  MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
 51  VGTQSGWDDG VGEDTVFVNV FGRIESLHV IVQTAYDNGN FAAQVHFFQ
101  NAIHAAVFGK RGFEFIHRFD ADLAFVIAQ CSGFDAGQK LYAFFSDVFG
151  FANCLIRRLG QACFAYPCLF LNAVLRD GNA VAAGGNIGMF GEKTHRIGID
201  VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRIRVG IEYGYFVAHG
251  FGSNSKHSAX*

```

m658/a658 75.3% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLVGTQSRGDDG					
a658	MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLRLLNVGTQSGWDDG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFRVESLHVIVQTAYDYGNTAQIHHFFQNAIHAAVFGKRGFEFIQCFY					
a658	VGEDTVFVNVFGRIESLHVIVQTAYDNGNFQAAQVHFFQNAIHAAVFGKRGFEFIHRFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFVAVQSRFQDAGQKLRFCSDFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT					
a658	ADLAFVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLGQACFAYPCLFLNAVLRD GNA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRFCQFVQSSLVVKRRRAQMAVGKFCRRVRIG					
a658	VAAGGNIGMFEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRIRVG					
	190	200	210	220	230	240
	250	260				
m658.pep	VENGYFVAHGFGNGKHSAX					
a658	IEYGYFVAHGFGSNSKHSAX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

g661.seq  
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT  
 51 GCGGGGCATT GCGGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG  
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT  
 151 ACCGGAAAAA CCctgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT  
 201 TGCCGTGCAG ATTGCCGGCA GCGACccga acaGATGGCG Gatgcggcgc  
 251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC  
 301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA  
 351 CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGcg  
 401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac  
 451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcattg ccgccCttgc  
 501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGCgcGTTAC  
 551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA  
 601 CCGCGACATC actTCgccc AAAAAGCCGC CGccgTCCTC AAACAAACCG  
 651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT  
 701 TTCCGCGATT TGAAGCATTA TGCCGAACAC GGCGTTTAC CGCCTGCCTT  
 751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCATATC CGCGCCATGC  
 801 ACGCGTTTTA TGGTGAAGACC GTCGGTGTGC GCATCGCAGC CAAACACATA  
 851 GGCTGGTACA TCGGCGAAAT GCCCGACGGC GAACAGGCGC GCGGTGA

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

g661.pep  
 1 MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN  
 51 TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC  
 101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQON  
 151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ  
 201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPFEAL CRTRRFTACL  
 251 EFGRMQSRHF EPHPRHARVL WXDRCARHRT QTHRLVHRRN ARRRTGAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

m661.seq  
 1 ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT  
 51 GCGGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG  
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT  
 151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT  
 201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC  
 251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT  
 301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA  
 351 CGAGCCGCTG GTTGCCGCCA TTTTGGGAAG CGTCGTCCGT GCGGCAGGCG  
 401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC  
 451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC  
 501 CGTCC.ACGG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC  
 551 GAACATCATC CCGAAACCAA ATGCCGCTG AACATCCCGG TCTGGGTCAA  
 601 CCGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG  
 651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC  
 701 TTCCGCGATT TGAAACATTA TGCCGAACAC GGTGTTTTC GCCTGCCTT  
 751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCATATC CGCGCCATAC  
 801 ACGCGTTTTA CCGCGACACC GCCGGTGTGC GCATCGCAGC CAAACACATA  
 851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

m661.pep  
 1 MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN  
 51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC  
 101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN  
 151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ  
 201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFACL  
 251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDDQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHDRARRARQAVVLPFRFETL					
g661	GALRTHRRDQKPSEHPGLGQRRHHFAAKSRRRPQTNRRRRHDRARRARQAVVFPRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCARHTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1   ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCGCCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCTCT AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCCT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1   MHIGGYFIDN PIALAPMAGI TDKPFRRLLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPFRFETL RRTRCFTACL
251 EFGRMRYHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					



1053

a661	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
	10 20 30 40 50 60
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
a661	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
	70 80 90 100 110 120
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
a661	VAAILEAVVKAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
	130 140 150 160 170 180
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
a661	SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
	190 200 210 220 230 240
m661.pep	CRTRCFAACLEFGRMRRRYFEPHPRHTVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
a661	RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
	250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTGCGTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAA g c c g c a A C C G C T A T C A C A A C G T C T T C C T T A T C G G G G C G C A C
501 CGAagggctg c g C G C C C t c g T C A A A C A G T T C C G C A A A A G C A G T G C G C C G T
551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTTGTG
601 GATTTTTTCG GCATtcagac GGCAACGATT ACCGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNNSVFN
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPIV READNTVTLO FYPAWSFSPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK REKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTTGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTTGAAACA

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1054

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201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TGCCTACCG CAATAAGCAT
301 TATTTGACG ACGCGCTGGC GCGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTG GGTTTTGTG
601 GATTTTTCG GTATTCAGAC GGCAACGATT ACCGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACC GTTTTA
801 GGTGCGCGAA CATCCGGAAC AATATTTTGT GCTGCACAAG CGTTTAAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51  KCFSEWSEEK RKTVLKQHFK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDIPLISMY S HQNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFE
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PV READNTVT LH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK					
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP RRRIGEINLAKCFPEWDEEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m663.pep	RKTVLKQHFKHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVILYPHFT					
g663	RKTVLKQHFKHMAKLMLEYGLYWYASAKCLKSLVRYRNKH YLDDALAAGEKVILYPHFT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m663.pep	AFEMAVYALNQDIPLISMYSHQNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
g663	AFEMAVYALNQDVPLISMYSHQNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m663.pep	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
g663	SAPFLYLPDQDFGRNNSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LQ					
	190	200	210	220	230	240
	250	260	270	280	290	
m663.pep	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHK RFKTRPEGSPDFYX					
g663	FYPAWSFPGEDAQADAQRMNRFIEERVREHPEQYFWLHK RFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAATT
51  TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCGCCGTA TCGGCGAAAT CAATTTGGCA

```

1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTG GGTTTTGTGTC
601 GATTTCTTCG GTATTTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCGT CTTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTTA TCGAGGAACG
801 CGTGCGCGAA CATCCCGAGC AGTATTTTTC GCTGCACAAG CGTTTCAAAA
851 CCCGTCGCGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAI PV READNTVTLH FYPAWESFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

```

          10      20      30      40      50      60
m663.pep  MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK
a663      MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFPEWDGKK
          10      20      30      40      50      60

          70      80      90     100     110     120
m663.pep  RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT
a663      RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT
          70      80      90     100     110     120

          130     140     150     160     170     180
m663.pep  AFEMAVYALNQDIPISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
a663      AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
          130     140     150     160     170     180

          190     200     210     220     230     240
m663.pep  SAPFLYLPDQDFGNRDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLH
a663      SAPFLYLPDQDFGNRDSVFVDFFGIRTATITGLSRIAALANAKVIPAI PVREADNTVTLH
          190     200     210     220     230     240

          250     260     270     280     290
m663.pep  FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
a663      FYPAWESFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
          250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGCTGAagg gGCGCACCGG ATGGGCGGTC
101 GGGCTGCGT CTCGGGGGAA CTGGTCTTGG CGCAGCAGGC GGATGTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGGAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TATTCTGTGC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTCCAT CGCGCCATA
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCgaagcgc gtttcgtcCc acttcatcgC gtTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT

```

551 GA

This corresponds to the amino acid sequence &lt;SEQ ID 2154; ORF 664.ng&gt;:

g664.pep

```

1  MIHPHHFRAF FINGHGVEIV HLLIADGAHR MGGRACVFGE LVLAQQADVL
51  DAAHGAAGAV AGKLLVAEHG QPFLQRKLEP VAAGYAVARP VVEIFVSDHG
101 FNAFEIGIGG GAAVGEDELG VKNVQTLVFH RAHIEIAYGD DHENIQVIFQ
151 PEARFVPLHR VFSTIPRQSR PWVCPLRWCK TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

m664.seq

```

1  GTGATACATC CGCACTACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGGCGG GCGCACCCGG ATGGGCGGTC
101 GGGCCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTT
151 GATGCGGCGC ACGGCGCGGC TGGCGCGGTC GCCGAAAAT TCTTGCTCGC
201 GGAAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TACTCGTGTG CGACCACGGA
301 TTCGATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCGCCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATCCAA
451 ACCGAAGCGC GTTTCGTCCC ATTTTCATCGC GTTTTT.CAA CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGAAA ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2156; ORF 664&gt;:

m664.pep

```

1  VIHPHYFRAF FINGHGVEIV HLLIAGGAHR MGGRACVFGE LVLAQQADVF
51  DAAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGYAVARP VVEILVSDHG
101 FDAFEIGIGG GAAVGKDELG VKDVQTLVFH RAHIEIAHGD DHENIQVVFQ
151 TEARFVPFHR VFXTIPRQSR PWACPLRWCK TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFF	FINGHGVEIV	HLLIAGGAHR	MGGRACVFGE	LVLAQQADVF	DAAHGAAGAV
	:	:	:	:	:	:
g664	MIHPHHFRAFF	FINGHGVEIV	HLLIADGAHR	MGGRACVFGE	LVLAQQADVL	DAAHGAAGAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m664.pep	AGKFLVAEHG	QPFLQRKLEP	VAAGYAVARP	VVEILVSDHG	FDAFEIGIGG	GAAVGKDELG
	:	:	:	:	:	:
g664	AGKLLVAEHG	QPFLQRKLEP	VAAGYAVARP	VVEIFVSDHG	FNAFEIGIGG	GAAVGEDELG
	70	80	90	100	110	120
	130	140	150	160	170	180
m664.pep	VKDVQTLVFH	RAHIEIAHGD	DHENIQVVFQ	TEARFVPFHR	VFXTIPRQSR	PWACPLRWCK
	:	:	:	:	:	:
g664	VKNVQTLVFH	RAHIEIAYGD	DHENIQVIFQ	PEARFVPLHR	VFSTIPRQSR	PWVCPLRWCK
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

```

1  GTGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TATCGGGCGG GCGCACCCGG ATGTGCGGTC
101 GGACCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTT
151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGAAAAT TCTTGCTCGC

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1057

```

201 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CTTGGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHFRAF FINGHGVEIV HLLISGGAHR MCGRTCVFGE LVLAQQADV
51  DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

**m664/a664** 92.9% identity in 183 aa overlap

```

              10      20      30      40      50      60
m664.pep    VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGGRACVFGEVLVAQQADVFDAAHGAAGAV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTCVFGEVLVAQQADVFDTAHGAAGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m664.pep    AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
              70      80      90      100     110     120

              130     140     150     160     170     180
m664.pep    VKDVQTLVFHRAHIEIAHGDHENIQVVFQTEARFVPFHRVFXTPRQSRPWACPLRWCK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a664         VKDVQTLVFHRTHIEIAHGDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
              130     140     150     160     170     180

m664.pep    TRFX
              ||||
a664         TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGg acgaaacgcg cttcgGggtg GAAtatgact tggatatatttT
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCAAGTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGCGGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCaacg CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCAGTTCG CCTGTGCGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
701 TGCCGCCAC GCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG .ACAGCGACG TTTCAGTGC TGGGAAGCCG

```

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1001 CCGCAACGCT CTACCGTCGC GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTGCGCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAa ctGTGGGACG GCACGGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCAggaaa
1301 accaaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTtctgt cctGCGCGCC GACCCCGCGC acatcgAAAC
1401 TGTTGCGGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTC AAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAaa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTTATCGGCT CAAGccgcgc cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCACAA
1651 GCGCGTTTCG TCATCGGCAG CTTAGCCGCG AACGTCCGCG ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCGCG TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTTCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

```

g665.pep
  1 MKWDETRFGL EYDLDFIMV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMVYK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNVFELTI KQTVPPTPDM ADKQPMMPV
251 KVGLLRNGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLYN PYSDDDLLLL LAHDSDAFTC WEAQAOTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROQA KQENQSYEYS PETADWRTL
451 NVCRAFVLR DPAHIETVAE KYGEMAQNMT HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLNPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

```

m665.seq
  1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
 51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAAGTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAAGTTC CCTTGTGGTA CAGCCAGGCG GGCACGCCCC TTTTGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCGCGATATG ACGGATAAAC AGCCGATGAT GATTTCCGTC
751 AAGTTCGGG TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTTCCT GCTGACCGAA GCCGAACAGA
851 CCTTCCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCGAAACGCT CTACCGCCG GCCGTGCGCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAG CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

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1059

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTGTCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTTCG TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAAGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCGG GCGCAGGAAG GATTGTGCGA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

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This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFMVV AVGFENMGAM ENKGLNIFNT KFVLADSRTA
 51 TDTFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTPVPTPDM TDKQPMMPV
251 KVGLLRNNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLATLS
351 DGVLEPKHEK LLAAVEKVIS DDLNDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLRA DPAHIETVAE KYGEMAQNM T HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEDEG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGLEYDLDFMVVAVGFENMGAMENKGLNIFNTKFVLADSRTATDTDFEGIES					
g665	MKWDETRFGLEYDLDFMVVAVGFENMGAMENKGLNIFNTKFVLADSRTATDTDFEGIES					
	10	20	30	40	50	60
m665.pep	VVGHEYFHNWVTGNRVTCRDWFQSLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNWVTGNRVTCRDWFQSLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNHOF					
	70	80	90	100	110	120
m665.pep	VVGHEYFHNWVTGNRVTCRDWFQSLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNWVTGNRVTCRDWFQSLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNHOF					
	70	80	90	100	110	120
m665.pep	PEDAGPTAHPVRPASYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGKMLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGKMLYFQRHDG					
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGKMLYFQRHDG					
g665	PEDAGPTAHPVRPVSYEEMNNFYTMVYEKGAEVVRMYHTLLGEEGFQKGKMLYFQRHDG					
	130	140	150	160	170	180
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPVPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPVPTPDM					
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPVPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPVPTPDM					
	190	200	210	220	230	240
m665.pep	TDKQPMMPVVKVGLLRNNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMMPVVKVGLLRNNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300
m665.pep	TDKQPMMPVVKVGLLRNNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR					
g665	ADKQPMMPVVKVGLLRNNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLHAHSDAFTRWEEAQTLYRRAVANLATLSDGVELPKHEK					
	:     :     :     :     :     :					
g665	GFSAPVYLNYPYSDDDLLLHAHSDAFTCWEEAQTLYRRAVANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
	:     :     :     :     :     :					
g665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMT					
	:     :     :     :     :     :					
g665	KWHELDROAAKQENQSYEYSPETADWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
	:     :     :     :     :     :					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	:     :     :     :     :     :					
g665	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
	:     :     :     :     :     :					
g665	CNKLEPHRKNLVKQELQCIHQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG ACGAAACGCG CTCGGTTTG GAATACGACT TGGATATTTT
51  CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGTGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGTACCGCC
151 ACCGATACCG ATTTGAAGG CATCGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTGACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGTTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCGGTGCG CCGTATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAAGTTC CCCGAAGACG CAGGTCCGAC CGCACATCCG GTGCGCCCCG
401 CCCGATATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGCGGAT GTATCACACC TTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGT ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCTGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGTGG ACGCGAACGG CATCAACCTC
601 GACCAATTCT CCTTGTGGTA CAGCCAAGCA GGTACGCCGG TTTTAGATGC
651 TCAAGGCGGT CTGAAAAACA ATGTGTTTGA GTTAACCATC AAACAAACCG
701 TGCCGCCAC GCGGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAATCGGGC TGCTGAACTG CAACGGCGAA GCGGTGGCAT TTGATTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCCAGTT CGAAAGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCGGTGCA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTTCTG CTCGCCCATG ACAGCGACGC CTTACGCGCG TGGGAAGCCG
1001 CACAAACGCT CTACCGCCGT GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCGTCG AGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC TTTCAAAGCC CTGCTTTTGG
1151 GTGTGCCGTC TGAAGCCGAG CTGTGGGACG GCGCGGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATATAC TTGCCGTCCG
1251 CTTTCTGCGG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAGTACAGC CCCGAAGCCG CCGGTTGGCG CACGCTGCGC
1351 AATGTCTGCC GCGCCTTCGT CCTGCGCGCC GATCCGCGCG ACATCGAAAC

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTTCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
  1 MKWDETRFGL EYDLDFIMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAENVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMIPIV
251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDL LLAHSDAFTR WEAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQRAA KQENQSYEYS PEAAGWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

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m665/a665 97.3% identity in 638 aa overlap

```

              10      20      30      40      50      60
m665.pep      MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
a665           MKWDETRFGL EYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFLVADSRTATDTDFEGIES
              10      20      30      40      50      60

              70      80      90      100     110     120
m665.pep      VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRR IENIRLLRQHOF
a665           VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRR IENIRLLRQHOF
              70      80      90      100     110     120

              130     140     150     160     170     180
m665.pep      PEDAGPTAHPVRPASYEEMN NFYTMTVYEKGAENVVRMYHTLLGEEGFQKGMKLYFQRHDG
a665           PEDAGPTAHPVRPARYEEMN NFYTMTVYEKGAENVVRMYHTLLGEEGFQKGMKLYFQRHDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m665.pep      QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM
a665           QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPTPDM
              190     200     210     220     230     240

              250     260     270     280     290     300
m665.pep      TDKQPMIPIVKVGLLN RGEAVAFDYQGKRATEAVLLLTEAEQTFLLGCVTEAVVPSLLR
a665           ADKQPMIPIVKIGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLR
              250     260     270     280     290     300

              310     320     330     340     350     360
m665.pep      GFSAPVHLNYPYSDDDL LLAHSDAFTRWEAAQTLYRR AAVANLATLS DGVELPKHEK
a665           GFSAPVHLNYPYSDDDL LLAHSDAFTRWEAAQTLYRR AAVANLAALS DGVELPKHEK
              310     320     330     340     350     360

```

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKGEMAQNMT					
a665	KWHELNRQAQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRIQAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQRIQAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCCTTGAA ACCGAACGTC ATTTCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCGCTGGTG
151 TTGGACGGTT CGGCAAAACT CTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCCTGTATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGCCCG
501 CCATTGGGTG AATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACCGTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGGTCCGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TATGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTAGGCGATT TCAATATGGG CCGGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCG CCGACAGCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCGGCGCGCG
1001 CCGTGCGCGC CATCGAGAAC ATCCGCTGTC TCGCCAGAAA CCAGTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TCGGGATGTA TCATACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTTCGCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTT TGGAAGCCGA AGCCCGTCTG
1351 AAAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCGGGCTTC
1451 TGAACCGCAA CGCGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGGCTT TCCCGCTCGA
1551 AGGTGTAACG GAAGCCGTCT TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCACGACA GCGACGCTT CACGTGCTGG GAAGCCGCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCT CAAAGCCCTG CTTTGGGCG TGCCGTCCGA
1851 AGCCGAACATG TGGGACGGCA CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCACAAT TGGACCGTCA GCGCGCGAAG CAGGAAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
2251 ATCGGCTCAA GCCGCCGCGAG CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCT GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG AATTGCAGTG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGCAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRSLTV EPQRAGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YLDLIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRTAT DTDPEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRVRRRIEN IRLLRQNQFP
351 EDAGPTAHPV RPVSYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPTPDMA DKQPMPIPVK VGLLRNNGEA VAFDYQGKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAEI WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTALQHP KFSLENPNKA RSLIGSFERN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVG E IVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTGACGGTT GAGCCGCAGA GGGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTGTGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGG ACAAACACCG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTT CAAACCGAGC TATCTGTTTG
551 CTTTGGTTCG GGGCGATTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGA TACGACTTGG ATATTTTCAT GGTCTGTCGC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAAA ATCCGCTTGC TCGCCAGCA CCAGTTCCCC
1051 GAAGACGCGAG GCCCGACCGC CCATCCGGTG CGCCCCGCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAGGAGGC GCGGAAGTAG
1151 TCGGGATGTA TCACACCCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCTT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCGGGA AGGTCGTCTG
1351 AAAACAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCCGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCG ACTATCAGGG CAAACGCGCG

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```

1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCGCCGCCA ACCTTGCCAC GCTTTTCAGAC GCGTTTGAGC
1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTTCAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTT CCGTCCACTT CCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCCG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCTT GCGCGCCGAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTT
2201 CCGACAAAGT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCTC
2251 GTCGGCTCAA GCGCGCCGAC GACACCCCTG CAACAGTTT GAACCGCCTT
2301 GCAGCATCCG AAATTTCAGC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGCGAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCCGC GCGCGCTTAG TGCAGCGCTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCAACG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

#### m665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFIMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQFSGDR ASRAVRRIEN IRLRQHQFP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYK EGVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPTPDMT DKQPMIPVK VGLLNNGEA VAFDYQKRA
501 TEAVLLLEA EQTFLLLEGV EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLPKHEKL LAAEKVISD
601 DLLDNAFKAL LLGVPSAEAL WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNROAAK QENQSYEYSP EAAGWRTL RNVCRAFVLRA PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
851 QEGLSKDVGE IVGKILD*

```

#### m665-1/g665-1 96.1% identity in 866 aa overlap

```

          10      20      30      40      50      60
m665-1.pep MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV LDGSAKLLSV
g665-1      MSKTVRYLKDY QTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV LDGSAKLLSV
          10      20      30      40      50      60

          70      80      90      100     110     120
m665-1.pep KINGAAADYV LEGETLTIAG VPSEFTVEV ETEILPAENK SLMGLYASGG NLFTQCEPEG
g665-1      KINGAAADYV LEGETLTIADVPSEFTVEV ETEILPAENK SLMGLYASGG NLFTQCEPEG
          70      80      90      100     110     120

          130     140     150     160     170     180
m665-1.pep FRKITFYIDR PDVMSKFTTT IVADKKRYPV LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS
g665-1      FRKITFYIDR PDVMSKFTTT IVADKKRYPV LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS
          130     140     150     160     170     180

          190     200     210     220     230     240
m665-1.pep YLFALVAGDL AVTEDYFTTMSGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL E
g665-1      YLFALVAGDL AVTEDRFTTMSGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL E
          190     200     210     220     230     240

          250     260     270     280     290     300
m665-1.pep YDLDFIMVVA VGDFNMGAMENK GLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT
g665-1      YDLDFIMVVA VGDFNMGAMENK GLNIFNTK FVLADSRAT DTD FEGIESV VGHEYFHNWT

```

1065

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
g665-1	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
g665-1	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
g665-1	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
g665-1	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
g665-1	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
g665-1	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
g665-1	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
g665-1	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
g665-1	790	800	810	820	830	840
m665-1.pep	850	860				
g665-1	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC  ATTTTGATAT TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTTGACGGTC  GAGCCGAAGA GGGTGGGAGA GCCGTGGTGTG
151 TTGGACGGTT CGGCGAAACT  CTTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG  AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTACG CGTCGAAGTG  GAAACCGAAA TCCTGCCGGC GGAACACAAA
301 TCGCTGATGC GGCTGTATGC  GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA  TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC  ATCGTCGCGG ACAAACACG CTATCCCGTT
451 TTGCTCTCCA ACGCAACAA  AATCGACGGC GGCGAGTATT CAGACGGCCG

```

```

501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTTG GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTGCGCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGGCGATT TCAATATGGG TCGATGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCCTTG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG TATCGAAAAC ATCCGCCTGC TCGCCAGCA CCAGTTCCCC
1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCCGCC GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTTACCT GCGACGATT
1251 CCGCGCGGCG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTGCGCT
1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGGCTCTG
1351 AAAACAATG TGTTCGAGT AACCATCAA CAAACCGTGC CGCCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA ATCGGGCTGC
1451 TGAAGTGAAG CGGCGAAGCG GTGGCATTG ATTATCAGG CAAACGCGCG
1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCCGTGCC GTGCCGCCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTT CAAAGCCCTG CTTTGGGTG TGCCGCTGTA
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGCGCGCGCA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCCG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAT CCGCGCACCA TCGAAAACCG TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCCGCCCTC
2251 GTCGGCTCAA GCGCCGCGAG CGACACCTG CAACAGTTT AAACCGCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAGGCC CGCTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGAGA AGACGGCAGC
2401 GGTACCCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTCGCC GCGCGCCTG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

#### a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSEFRTVEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRHQHFP
351 EDAGPTAHPV RPARYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPPTPDMA DKQPMMPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVELPKHEKL LAAVEKVISD
601 DLLDNAFAKAL LLGVPSEAEL WDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNROAAK QENQSYEYSP EAAGWRTLRL VCRAFVLRAD PAHIETVAEK
701 YAEQAQNMTH EWGILSAVNG NESDTRNRL AQAADKFSD ALVMDKYFAL
751 VGSRRSDTL QOVQALQHP KFSLENPNKA RSLIGFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV					
	:     :     :					
m665-1	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV					
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSERFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSERFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFS DGRHWVKWEDPFSKPS
	130 140 150 160 170 180
a665-1.pep	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGF AVESLKNAMKWDETRFGLE
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGF AVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	YDLDFIMVVAVGDFNMGAMENKGLNIFNTK FVLADSRATDTDFEGIESVVGHEYFHNWT
m665-1	YDLDFIMVVAVGDFNMGAMENKGLNIFNTK FVLADSRATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRR IENIRLLRQHQPEDAGPTAHPV
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRR IENIRLLRQHQPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	RPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA
m665-1	RPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	MVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPTPDMADKQPMMPVK
m665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDMTDKQPMMPVK
	430 440 450 460 470 480
a665-1.pep	IGLLNCNGEAVAFDYQGKRATEAVLLL TEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
m665-1	VGLLNRCNGEAVAFDYQGKRATEAVLLL TEAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	YSDDDLLLLLAHSDAFTRWEEAAQTL YRRAVAANLAALSDGVLPKHEKLLAAVEKVSD
m665-1	YSDDDLLLLLAHSDAFTRWEEAAQTL YRRAVAANLATLSDGVLPKHEKLLAAVEKVSD
	550 560 570 580 590 600
a665-1.pep	DLLDNAFKALLGVPSEAE LWDGAENIDPLRYHQAREALLDILAVRFLPKWHELN RQA AK
m665-1	DLLDNAFKALLGVPSEAE LWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELN RQA AK
	610 620 630 640 650 660
a665-1.pep	QENQSYEYSPEAAGWRTL RNVCRAFVLRADPAHIETVAEKYAEMAQNMTHEWGILSAVNG
m665-1	QENQSYEYSPEAAGWRTL RNVCRAFVLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	NESDTRNRLLAQFADKFSD DALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
m665-1	NESDTRNRLLAQFADKFSD DALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	RS LIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
m665-1	RS LIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	790 800 810 820 830 840

1068

	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQRI	RAQEGLSKDVGEIVGKILD	X			
m665-1	VKQALQRI	RAQEGLSKDVGEIVGKILD	X			
	850	860				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1   ATGCTTTGTA TGAATTATCA ATCAAACCTCA GCGGAAGGAG TGCTTGTAGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGGTGGTG CATTGTGTGT GTATTGGGAC AATACCGCCA
401 AACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1   MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTHSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1   ATGCCTTGTA TGAATCATCA ATCAAACCTCA GCGGAAGGAG TGCTTGTGGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGGTGGTG CATTGTGTGT GTATTGGGAT AATACCGCCA
401 AACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1   MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

	10	20	30	40	50	60
m666.pep	MPCMNHQSNS	GEGVLVAKTY	LLTALIMSMT	ISGCQVIHAN	QGKVNTHSAV	ITGADAHTPE
g666	MLCMNYQSNS	GEGVLVAKTY	LLTALIMSMV	ISGCQVIHAN	QGKVNTHSAV	IAGADAHTPE
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQ	VIASDFIVAS	ANPLATQAGY	DILKQGSAA	DAMVAVQTTL	SLVEPQSSGL



[illegible]

```
a666.seq
  1  ATGCCTTGTA  TGAATCATCA  ATCAAACCTCA  GGCGAAGGAG  TGCTTGTTGGC
51  TAAAACATAT  TTATTGACTG  CATTGATAAT  GTCTATGACA  ATCTCTGGAT
101 GTCAAGTCAT  CCATGCCAAT  CAAGGTAAGG  TTAATACTCA  TTCTGCTGTC
151 ATCACAGGTG  CAGACGCTCA  CAGCGCTGAA  CATGCAACGG  GACTGACCCA
201 ACAAAGCAG  GTGATTGCAA  GTGATTTTAT  GGTAGCGTCA  GCAATCCAT
251 TAGCAACACA  AGCTGGCTAT  GATATCTTAA  AGCAAGGCGG  TAGCGCTGCA
301 GATGCGATGG  TGGCGGTGCA  GACGACACTA  AGCTTGGTAG  AGCCACAGTC
351 GTCAGGCTTG  GGCGGTGGTG  CATTTGTGTT  GTATTGGGAT  AATACCGCCA
401 AAACATTGAC  CACATTTGAT  GGGCGTGAGA  CGGCACCGAT  GCGTGGAACG
451 CCGGAATTAT  TTTTGGATAA  AGATGGTCAA  CCATTGCAAT  TTATGGAAGC
501 GGTGGTCGTG  GTCGCTCGGT  GGGTACGCCT  GCTATCCCTA  AACTGA
```

```

a666.pep
1  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51 ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGGSA
101 DAMVAVQTTT SLVEPQSSGL GGAFAVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGG PLKFMEAVVV VARWVRLLSL N*

```

		10	20	30	40	50	60
m666.pep		MPCMNHQSNSEGGVVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHTSAVITGADAHTPE					
a666		MPCMNHQSNSEGGVVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHTSAVITGADAHTPE					
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLTSLVEPQSSGL					
a666		HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLTSLVEPQSSGL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDQPLKFMEAVVVVARWVRLLSL					
a666		GGGAFVLYWDNTAKTLTTFDGREAPMRATPELFLDKDQPLKFMEAVVVVARWVRLLSL					
		130	140	150	160	170	180
m666.pep		NX					
a666		NX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1   atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAAttgcg
151 GAtttccttc agcgtgcccg cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCAG ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggtcG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GGC GTTATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCAACCACT TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ACtTGCGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1   MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQRRARVER FPFHAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVAE IAVARIPIAR GVDVYQGA V MQYQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNLVLP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHFVIRQGR RQVIQRTDTL HIGYGFNIES
251 QNRIHGSTLH SKTDLRL LCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCCGCTT GTGCGGACAG GTAATCCGC ATCCGTTTGA
51  TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCTTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTGCCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGC GTTATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACGCCGCC
451 GTTCCAACTG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTAT CCTGCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCAACCACT TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVAE IAVAHIPIAR GVDVYQGA V MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHL
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

              10      20      30      40      50      60
m667.pep    MRLFPGLCGQVIPHPDFHFVVRIQPAADQTETQVHQISVCRVGFALIA DFLQPARMEC
              ||:  | |: :  | ||: |||: : ||| |||: ||| :  : ||| ||| ||| ||: |
```

g667	MRFVFCLGGEIVSDPCDFHLVFRVESAADQTTETQIHQIRIHGIGFAIIADFLQRARVER	10	20	30	40	50	60
m667.pep	LPNLAAVHTQLARKTAQFRHIVQRHVCFRLVKREQIHQIAVALVITADVVPLEIAAAVE	70	80	90	100	110	120
g667	: :: :     :     : :     :     :     :     :     :     :						
	FPHFAAVHTQLARKAAQFRHIVQRHIRPRLVKREQIHQIAVALVITADVVPLEIAAAVE	70	80	90	100	110	120
m667.pep	IAVAHIPIARGVDVAVYQGAVMQYGGIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD	130	140	150	160	170	180
g667	: : :     :     :     :     :     :     : : : : : : : : : :						
	IAVARIPIARGVDVAVYQGAVMQYGVETAAVPADQLRRMFFNQFEKLGNHDFFAIVHLAD	130	140	150	160	170	180
m667.pep	GADMYFILPPTHAARNRHNLMKMMLHKIAARLSTAFVLGNQHHL	190	200	210	220		
g667	: :						
	GADMNLVLPAAHTAGNRHNLMEEVLHKIAAGLCAAFLLREQHGFVIRQGRRQVIQRTDTL	190	200	210	220	230	240
g667	HIGYGFNIESQNRIHGSTLHSKTDLRLLLCHX	250	260	270			

```
a667.seq
1 ATGCGGTTTG TCTTCTGT TT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51 TTTCCATTTC GTATTCTGCT GCGTCGAATC TGCCGCTGAC CAGACAGAA
101 CGCAGATACA TCAGATAGGT ATTTACCGCA TCGGTTTTCG AATAATTGCG
151 GATTTCTCTC AGCCTGCCCG CGTGGAACGC CTCCCACACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTTC CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGCG
351 TGTCGCCGAA ATCGCCGTCG CCGATATCCC AATAGCGCGC GGGCTTGATG
401 CCGTGTAGCA GCGAACGGTA ATGCAGAACC GGCAGGTCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCTCTG CCGTCATCCA TCTCGCCGAT TGTACCGACA
551 TGGACTTTAT CTTGCCCCCA ACGCATGCGC CAGCAAAATCG CCACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAA CAGCACCCT TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACACGCTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGTTT TTA AAA.CAG ACTTGCGCCT
801 AATGTGTCAT TAA
```

```
a667.pep
1  MRFVFC LGGE  IVSDPLDFHF  VFVCVESAAD  QTETQIHQIG  IYRIGFAIIA
51  DFLQPARVER  LPHLAAVHTQ  LARKTAQFRH  IVQRHIRPRL  VKREQIHQIA
101 MTLVVAADV  VPLEIAAAVE  IAVAHIPIAR  GVDV*QRTV  MQNRQVETAA
151 VPTDQLRRMF  FNQLEKFGDN  HFLAVIHLAD  CTDMDFILPP  THAARNRHNH
201 MKMMLHKIPT  RLSTAFLLGK  QHHFIVGQRG  RQVIQRTDTL  HIGYGFNIES
251 ONRGHSDSTLY  LKXDRLLLCH  *
```

[illegible]

	70	80	90	100	110	120
	130	140	150	160	170	180
m667.pep	IAVAHIPIARGVDVAVYQGAVMQYGGIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD					
	:     :     :     :     :					
a667	IAVAHIPIARGVDVAVXQRTVMQNRQVETAAVPTDQLRRMFFNQLEKFGDNHFLAVIHLAD					
	130	140	150	160	170	180
	190	200	210	220		
m667.pep	GADMYFILPPTHAARNRHNLMKMMHLHKIAARLSTAFVLGNQHHL					
	:  :     :     :     :     :					
a667	CTDMDFILPPTHAARNRHNLMKMMHLHKIPTRLSTAFLLGKQHHEFIVGQRGRQVIQRTDTL					
	190	200	210	220	230	240
a667	HIGYGFNIESQNRGHDSTLYLKXDLRLLLCHX					
	250	260	270			

```
g669.seq
1  ATGCGCCGCA TCGTTAAAAA ACACCAGCCG GTAAACGCGC CACATATCGT
51  TTTGGAATTT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACAGTTC CCATCATCAT GACCGCAGCC TTCGGCGGCA ATCAGGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTAC AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGACTACTGA A
```

g669.pep  
1 MRRIVKKHQF VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI  
51 EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA  
101 DIKRIL\*

```
m669.seq
1 ATGCGCCGCA TCATTA AAAA ACACGAGCC ATAAACGCGC CACATATCGT
51 TTTGGA AATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTC CCGATCATCAT GACAGCAGCC TTCGCGCGCA CACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACAG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTTCG TTACAATGCC
301 GACATCAAAC GGATACTGTA A
```

```
m669.pep
  1  MRRIIKKHQP INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHGI
 51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQ TAL SRPAVFGYNA
101  DIKRIL*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m669.pep	MRRRIKKHQPINAPHIVLEIRIMKLHRAVFVFLGRKRPHHHDS	SLRRQHGIEGMGDFKQI				
	:       :       :       :       :       :	:       :       :       :       :       :				
g669	MRRIVKKHQPVNAPHIVLEIRIMKLHRAVFVFLGRKRPHHHDRS	LRRQHGIEGMGDFKQI				
	10	20	30	40	50	60
	70	80	90	100		

1073

```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT TCAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATT TACGCCCTG CCGTTTTTCG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIKKHQP VNAPHIVLEI RIMKLHRAV FLGRKRPHH DRSLRRQHGI
51 EGMGDFKQI FRHVQSSNRQ NGRQPVCTK PNTASLTAL SRPAVFGYNA
101 DIKRIL*

```

**m669/a669** 98.1% identity in 106 aa overlap

```

m669.pep    10      20      30      40      50      60
             MRRIKKHQPINAPHIVLEIRIMKLHRAVFLGRKRPHHDSLRRQHGI EGMGDFKQI
             |||||:|||||
a669        10      20      30      40      50      60
             MRRIKKHQPVNAPHIVLEIRIMKLHRAVFLGRKRPHHDSLRRQHGI EGMGDFKQI

m669.pep    70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTGAA
51 AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCTGTTC GCATTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTACAGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTAA
51 AAACGCTTCG GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCGTCA AACACATTA

```

1074

```

251 CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

m670.pep	10	20	30	40	50	60
	MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITSATSRANPISWVTHIIVMPLSAKS					
g670	MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITSATSRANPISWVTHIIVMPLSAKS					
	10	20	30	40	50	60
m670.pep	70	80	90	100	110	120
	FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
g670	FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCWPPESWEGKASFLCASPTRSK					
	70	80	90	100	110	120
m670.pep	130	140	150			
	SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX					
g670	SSIAFFSACS AFCPLTFIGARVMSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGTTGTA
 51 AAACGCTTCC GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGTTCGA GTGCGGAGGT CGGTTTCGTC AACACATTA
251 CGCGCGGTTT CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCCATCG CTTTCTTCTC TGCTGTTC GCATTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

m670.pep	10	20	30	40	50	60
	MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITSATSRANPISWVTHIIVMPLSAKS					
a670	MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITSATSRANPISWVTHIMVIPLSAKS					
	10	20	30	40	50	60

1075

	70	80	90	100	110	120
m670.pep	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.pep	SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX					
a670	SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAAcAgg cggggTTGGA ACGagcAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGaaggAAA
251 ccaccCATGC cACCATCgaa cctGCTTCGG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTCTGTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGAAKSLAK KKETTHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAAcAGG CGGGGTTGGA ACGAGGCAAA
201 GGCGAGGTcG GCGAAGGAGG CGGCaaAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTGCGCAAT
351 GGGGAGGCTA TTCATTCTGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR					
g671	MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRSMGRL					

1076

```

|||||
g671  RGWNEAKARS AKGA AKSLAKKKETHATIEPASAITPRIVEMTMQAAMTAEARRSAMGRL
      70      80      90      100     110     120

      130      140      149
m671.pep FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
|||||
g671  FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
      130      140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2199>:

```

a671.seq
1  ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCCCCGG
101 TCAGCAGCGA GCGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTGGGA ACGATGCAAA
201 GCGCATGTCT GCGAAGGGTG CCGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGATGGCG GAGACGAGGA GGTCCGCAAC
351 GGGGAGGTTA TTCATTCGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2200; ORF 671.a>:

```

a671.pep
1  MTSRVIIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNDAKAMS AKGA AKSLAK KKATTHAAIE PASAITPRIA
101 DSTMQAAMMA ETRRSATGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

m671/a671 93.9% identity in 148 aa overlap

```

      10      20      30      40      50      60
m671.pep MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR
|||||
a671  MTSRVIIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDANANR
      10      20      30      40      50      60

      70      80      90      100     110     120
m671.pep RGWNEAKARSAKEAAKSLAKKKETHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL
|||||
a671  RGWNDAKAMSAKGA AKSLAKKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL
      70      80      90      100     110     120

      130      140      149
m671.pep FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
|||||
a671  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
      130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2201>:

```

g672.seq
1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTATC GACATCATTA AAGCACAAA AATCGCCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTCTGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAT GCATTCTGCC GGCAGTTCGA CCGCCCTAT
301 ATTAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC AACGCTCAGG CACTGCTGTT CGATGCCTAT CACCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGact GGacgctgtt ggcggAATAT
451 TCGGGCAAGC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCCG
501 CGAAGCCGTC CGCATCACCG GAGCGGAAGC GGTGACGTA TCCGGCGGCG
551 TGAAGCGTC TAAAGGCAAA AAAGACCCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA

```



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

Computer analysis of this amino acid sequence gave the following results:

**m672/g672** 91.3% identity in 208 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1078

```

1   ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCGCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAGCCC  CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC  CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC  CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA  CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA  TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC  GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG  CACCGGACAC CGCTTCGACT GGACGCTGTT GGCGGAATAT
451 TCGGGCAAAC  CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC  CGCATCACCG GAGCGGAAGC GGTCTGATGTA TCCGGCGGCG
551 TGGAAGCGTC  TAAAGCAAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACGCCCA  ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1   MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAV DIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

```

              10      20      30      40      50      60
m672.pep      MRKIRTKICGITTPEDAAGADAVGLVFFQGSRAVDIARAKKITAALPPFVSVVA
              |||||:||||: |||||:||||: |||||:||||: |||||:||||:
a672           MRKIRTKICGITTPEDALYAAHAGADALGLVFYQSPRAVDIKAQKITAALPPFVSVVA
              10      20      30      40      50      60

              70      80      90      100     110     120
m672.pep      LFNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF
              |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
a672           LFNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRFP
              70      80      90      100     110     120

              130     140     150     160     170     180
m672.pep      DAQALLFDAYHPSEYGGTGNRFDWTLLEYSGBKPWVLAGGLTPENVGEAVRITGAESVDV
              |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
a672           DAQALLFDAYHPSEYGGTGNRFDWTLLEYSGBKPWVLAGGLTPENVDEAIRITGAEAVDV
              130     140     150     160     170     180

              190     200     209
m672.pep      SGGVEASKGKKDAAKVAEFIATANRLSRX
              |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:||||:
a672           SGGVEASKGKKDPKVAEFIATANRLSRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1   ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CCGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGAAA  CAACTGCCCA AGCACAGCC GGTCAATTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCGTTTGT
451 GCCCAAGTGC GCGCCGAATT TGAATTTCG GCGCGGAGG CGGTCAAGTC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTTCGT GAAAACTCT TCCGCTATTT

```

1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGCATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCCTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

m673.pep      10      20      30      40      50      60
MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
|||||
g673          10      20      30      40      50      60
MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI

m673.pep      70      80      90     100     110     120
YTDDTAQFVFVDTPGFQTDHNRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK
|||||

```

[illegible]

```
a673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCC GTATTACGAC CAAAAGGCG
151 CAGACGACGC CAGACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGCGTGGAT
301 GTGGTGGTTT TCGTCTGTGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGTAAA CAAGTCCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT AGCGCGTGGA CGCGTTTGTT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGCG
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGT TCGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG
```

a673.pep

1	MDIETFLAGE	RAADGYRCGF	VAIVGRPNVG	KSTLMNHLIG	QKISITSKKA
51	QTTRNRVTGI	YTDDTAQFVF	VDTPGFQTDH	RNALNDRLNQ	NVTEALGGVD
101	VVVFVVEAMR	ETDADRVLK	QLPKHTPVIL	VVNKIDDKKA	KDRYALEAFV
151	AQVRAEFEFA	AAEAVSAKHG	LRIANLLELI	KPYLPESVPM	YPEDMVTDKS
201	ARFLAMEIVR	EKLFRYLGE	LPYAMNVEVE	QFEEDDGLNR	IYIAVLVDKE
251	SQKAILIGKG	GERLKKISTE	ARLDMEKLFD	TKVFLKVWVK	VKSGWADDIR
301	FLRELGL*				

```

          10          20          30          40          50          60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          |||||
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          10          20          30          40          50          60

```

1081

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRNLNQNVTEALGGVDVVVFVEAMRFTDADRVVLK					
a673						
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEFAAAEAVSAKHGLRIANLLELI					
a673						
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673						
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGGGERLKKISTEARLDMEKLFDTKVFLKVVVKVKS GWADDIR					
a673						
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673						
	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCCG CGAAATGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETYPY
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCCG CGAAATGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCGGCAGAG TATATCCGAC AAATCCGCCC
201 GTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCCGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

51 FFGTQTNAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP  
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	::					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAAACAG	CCCGCCGCCG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCCGAAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TCGTCAACG	GCATCCTCGA	CAAACCTGCC	GCCCCAAATCC
401	GTCCCGACGA	GCCCCAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcacgctc
151 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC
201 CTCTTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep  
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV  
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI  
 101 GRVALDYNIP IANAVLT TEN DAQAIERIGE KASDAKVAV ECANLVNLLL  
 151 EEQFEDEE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq  
 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT  
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT  
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC  
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC  
 201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG  
 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC  
 301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC  
 351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG  
 401 ATGCCGCCAA AGTCGCGCTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC  
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep  
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV  
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV  
 101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAKVAV ECANLVNLLL  
 151 EEQFEDEE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE LVSNEGAGVSRVALDYNIP IANAVLT TEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFE LVANESGAGIGRVALDYNIP IANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq  
 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT  
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT  
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC  
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC  
 201 CTCTTCTGAA AAATTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG  
 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC  
 301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC  
 351 CACGGAAAAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG  
 401 ATGCCGCCAA AGTCGCGGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC  
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep  
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV  
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV



1085

101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAKVAV ECANLVNLLL  
 151 EEQFEDEE\*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq  
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg  
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCCGGCGT  
 151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGG CAACGCGCCA  
 201 ACGGCGAAAT CCAAGAAATT TTGTTTGGCG CGGTATCGAT TTCATCGACG  
 251 CCGACGATT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC  
 301 GGTGCGGCGG AAAAATACTT GGTGCGTTCG TCGCGCAAT TCGGGATCGA  
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG  
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG  
 451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
 551 GCGTAATGT AGTTTGTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep  
 1 MPQILVRIFL IRYSEFIWTV RLCRFRRHSR SVDFDVFDK DFNFLTAFRR  
 51 VQNHVAFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT  
 101 GRAEKYLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA  
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq  
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTG  
 51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCCGGCGT  
 151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGA CAACGAGCCA  
 201 GCGGCGAAAT CCAAGAAATT TTGTTTGGCG CGGTATCGAT TTCATCGATG  
 251 CCGACGATT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC  
 301 CGTCGCGCGG AAAAACACTT GGTGCGTTCG TCGCGCAAT TCGGGATCGA  
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG  
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG  
 451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
 501 CTTTGTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
 551 GCGTAATGT AGTTTGTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep  
 1 MPQILVRIFL IRYSEFIWETA RLCRFRRHSR SVDFDVFDK DFNFLTPFRR

```

51  VQNHFVAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
151 VAVACRPVDD LDDEGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

```

              10      20      30      40      50      60
m677.pep      MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLTFFRRVQNHVAFAR
              |||||
g677           MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDRKDFNFLTAFRRVQNHVAFAR
              10      20      30      40      50      60

              70      80      90      100     110     120
m677.pep      FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
              |||:|
g677           FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGDRAEKYLVRFAQFGIDDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.pep      SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
              |||||
g677           SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.pep      PSGGRNVVFGFGTHIVCGX
              |||||
g677           PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

```

a677.seq
1  ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
51  GGAAACGCGC CGTTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGGCGT
151 GTTTAAACCC ACTTCGTCGC CTTACGCGC TTTAATCAGA CAACGAGCCA
201 GCGGCGAAAT CCAAGAAATT TTGTTTTCGC CGGTATCGAT TTCATCGATG
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
301 GGTGCGCGCG AAAAACACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCAA
351 CGACGACGGC GGCTTCCAAA CGCTTGGTCA GGAAACGGAT GCGGCGGTGC
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGG TAGTCGCCGT TTTGCTGCG
451 GTCGCCGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
501 CTTTATTAAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
551 GGCCTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

```

a677.pep
1  MPQILVRIFL IRYSEFIWETA RLCRFRHRSR SVDFDVFDRK DFNFLTFFRR
51  V*NHFVAFTR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
101 GRAEKHLVGR FAQFGINDDG GFQTLGQETD AAVDFAHTAF AVKVVAVFAA
151 VAVACRPVDD LDDEGAFFIN QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

```

m677/a677 93.4% identity in 198 aa overlap

```

              10      20      30      40      50      60
m677.pep      MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLTFFRRVQNHVAFAR
              |||||
a677           MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDRKDFNFLTFFRRVXNHVAFTR
              10      20      30      40      50      60

              70      80      90      100     110     120

```

1087

```

m677.pep      FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQSDRRAEKHLVGRFAQFGIDDDG
                |||||||||||||||||||||||||||||||||||:|:| |||||||||||||||:|
a677          FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTDRRAEKHLVGRFAQFGINDDG
                70      80      90      100      110      120

                130      140      150      160      170      180
m677.pep      SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDLDFGAFFVDQLIKLVFQCL
                :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a677          GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDLDFGAFFINQLIKLVFQCL
                130      140      150      160      170      180

                190      199
m677.pep      PSGGRNVVFGFGTHIVCGX
                |||||||||||||||
a677          PSGGRNVVFGFGTHIVCGX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1   ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTcgcCGG TCATCGCCCGC
51  CTGCATCGTC ATTTCCACGA TCGCGGCGGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggtTTcc tTCTTTTtg ccAAACTCTt tGCCGCACcc
151 ttcgcgcACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCCGTCT GGGCTTTGCC
301 AACCGCATT TGGGCGGTGT ATTCGGTGCA TTGAAAGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1   MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51  FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1   ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCCGC
51  CTGCATCGTG CTATCCGCGA TCGCGGCGGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTCTGTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCCGTCT GGGCTTTGCC
301 AACCGCATT TGGGCGGCGT ATTCGGTGCA TTGAAAGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1   MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51  FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m678/g678** 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFALFAASFADLAFASFQ					
	:     :     :     :     :					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFALFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	:     :     :     :     :					
g678	PRLFALALSFISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	:     :     :     :     :     :					
g678	IMLASKTDLPDTEEWQSYTVFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGC GCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTT TTTTCG CCAA ACTCTT TGCCGCACCC
151 TTCGCGGACA TCGCCTTTGC ATCGTTCCAA CCCC GCCTGT TTGCATGGGC
201 TCTGTCTGTC ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLEAAP
51 FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGILITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFALFAASFADLAFASFQ					
	:     :     :     :     :					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFALFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	:     :     :     :     :					
a678	PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	:     :     :     :     :					
a678	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51 GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```

1089

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAAACTGA TGTTTTTCTG TTTCACATGG TCGAGCAGCC
551 GTCCGACGGT GCGGACGACT ATTTGCGCAG CCGCACGCAG GTCGGCGGTT
601 TGTTTGTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMMFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51 GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCGCTT CTGAATGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GCGGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATAAGGTCT GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGGACGACG ATTTGCGCAG CCGCACGCAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90     100     110     120
m680.pep TLCLVLQNTMTWFICKSTISRSSRLRFKXVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||||:|||||:|||||
g680      TLCLVLQKTTITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          70      80      90     100     110     120

          130     140     150     160     170     180
m680.pep ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLKFWMFCFTW

```

1090

```

|||||
g680      ASLRIGAEKVAEKSRVWRWRGSICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW
           130      140      150      160      170      180

           190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNTVWRSGRFLMX
           |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVCRSGRFLMX
           190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1  ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCCGCGCGG CGATATCGGT
51 GCGCAGCAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTCTTGCGC GGCGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGACGCC
551 GTCCGACGGT GGCGACGACG ATTTTCGCAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

           10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
           |||||:|||||:|||||
a680      MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
           10      20      30      40      50      60

           70      80      90      100     110     120
m680.pep  TLCLVLQNTMTWFICKSTISRSSRLRFXMVSTAMMCCSTLALVVCAATSTVSGAFMKSC
           |||||
a680      TLCLVLQNTMTWFICKSTISRSSRLRFXMVSTAMMCCSTLALVVCAATSTVSGAFMKSC
           70      80      90      100     110     120

           130     140     150     160     170     180
m680.pep  ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
           |||||
a680      ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW
           130     140     150     160     170     180

           190     200     210     220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNTVWRSGRFLMX
           |||||
a680      SSSRPTVATTISQPARRSAVCLSIFIPPNTVWRSGRFLMX
           190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA
51 GTTCATCAGC GCGATGGGGA TTCAAGCGC GCCGGGTACG GTGGcgacgg

```

```

101  tgatgtTTTC  GTCTGCTACG  CCCAATTCTT  GGAGGGTGCG  GCAGCAGACT
151  TTGAGCATT  GGCTGCCGAT  TTCGTTGGTG  AAGCGTGCCT  GTACGATGCC
201  GATGCGGAGG  TGTTTGCCgt  cgaggttgGG  GGCGATGGTG  TTCATTGGGT
251  GTCCTTTGGT  ATTCGGGGTT  TCGGAATGCC  GTCTGAAGGT  TTCAGTCTTG
301  CGGCTGCCAG  TCGGCAACGG  TTTGGAATGT  GCCGTCTTCG  GCAAGCTCCC
351  ACGCGTGCC  TTCGGGTTGG  GAAAGCAGTG  CGGCGGTTTC  AGGGTTGGTT
401  TTGGTGATGT  CGGCGAGGCT  GACGATGCTG  AAGTTGTCCG  GGTCGTCGGT
451  GTATTCGTCG  GTTTCGTCGC  CGCTGAAGAA  ACGCCAGCCG  CTGTCGTTTT
501  CAAAAACGGG  GGCTTCGCGG  TAAAGGAAGC  CGACGGGCCG  GTTTTGTTTG
551  GCGACGGTGT  TGGTGGCGAT  GCAGCGGTCG  AGTGCCGAGG  AAAGTGCTTG
601  TGCAAATGCG  TTCATTGCGG  GAATACGTTG  GGGGGGGGGA  AACTTGCGGA
651  TTTTACCACG  ATTCCCGCGT  TGTCGGCAGA  CGGCGGCGGT  TTGGTGGTAC
701  AATGTGCGCC  GTTTGCAGCC  TTAAGGTGTT  TCTGTATTTT  TGGAGTATGG
751  AAACGCATTC  GGGCTGTTTT  TTGCGGAAGA  CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

**g681.pep**

```

1  MTTTPMAISAS  NFSEEAKFIS  AMGISSAPGT  VATVMFSSAT  PNSWRVRQQT
51  LSIWLPISLV  KRACTMPMRR  CLPSRLGAMV  FIGCPLVFGV  SECRLKVSVL
101 RLPVGNGLC  AVFGKLPRAA  FGLGKQCGGF  RVGFGDVGEA  DDAEVVGVVG
151 VFVGFVAEE  TPAAVVFKN  GFAVKEADGP  VLFGDVGVD  AAVECRGKCL
201 CKCVHCGNTL  GGGKLADFTT  IPALSADGGG  LVVQCAPFAA  LRCFCIFGVW
251 KRIRAVFCGR  R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

**m681.seq**

```

1  ATGACGACGC  CGATGGCAAT  CAGTGCCTCA  AACTTTTCGG  AAGAGGCAAA
51  GTTCATCAGC  GCGATGGGGA  TTTCAAGCGC  GCCGGGTACG  GTGGCGACGG
101 TAATGTTTTT  GTCTGCCACG  CCCAATTCTT  GGAGGGTGCG  GCAGCAGACT
151 TTGAGCATT  CGCTGCCGAT  TTCGTTGGTG  AAGCGTGCCT  GTACGATGCC
201 GATGCGGAGG  TGTTTGCCGT  CGAGGTTGGG  GGCGATGGTG  TTCATTGGGT
251 GTCCTTTGGT  ATTCGGAGTT  TCGGAATGCC  GTCTGAAGGT  TTCAGTCTTG
301 CGGCTGCCAG  TCGGCGACGG  TTTGGAATGT  GCCGTCTTCG  GCAAGCTCCC
351 ATGCGCTGCC  TTCGGGTTGG  GAGAGCAGTG  CGGCGGTTTC  AGGGTTGGTT
401 TTGGCGATGT  CGGCGAGGCT  GACGATGCTG  AAGTTGTCCG  GATCGTCGGT
451 GTATTCGTCG  GTCTCGTCGC  CGCTGAAGAA  ACGCCAGCCG  CTGTCGTTTT
501 CAAAAACGGG  GGCTTCGCGG  TAGAGGAAGC  CGACGGGCCG  GTTTTGTTTG
551 GCGACGGTGT  TGGTGGCGAT  ACAGCGGTCG  AGTGCCGAGG  AAAGTGCTTG
601 TGCAAATGCG  TTCATTACGG  GAATACGTTG  GGGG.AAAAC  TTACGATT
651 TACCACGATT  CGTGCGTTGT  CGGCAGACGG  CGGCGGTTTG  GTGGTACAA
701 GTGCGCCGTT  TGCAGCCTTA  AGGTGTTTCT  GTATTTTGG  AGTATGGAAA
751 CGCATTCGGG  CTGTTTTTTG  CGGAAGACGG  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

**m681.pep**

```

1  MTTTPMAISAS  NFSEEAKFIS  AMGISSAPGT  VATVMFSSAT  PNSWRVRQQT
51  LSIWLPISLV  KRACTMPMRR  CLPSRLGAMV  FIGCPLVFGV  SECRLKVSVL
101 RLPVGDGLEC  AVFGKLPCAA  FGLGEQCGGF  RVGFGDVGEA  DDAEVVRIVG
151 VFVGLVAEE  TPAAVVFKN  GFAVEEADGP  VLFGDVGVD  TAVECRGKCL
201 CKCVHYGNTL  GXKLDTFTI  RALSADGGGL  VVQCAPFAAL  RCFCIFGVWK
251 RIRAVFCGR  *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

**m681/g681**

```

          10      20      30      40      50      60
m681.pep  MTTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPLISLV
          |||||
g681       MTTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPLISLV
          10      20      30      40      50      60

```

1092

	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVG DGLECAVFGKLPCAA					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGNGLECAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVFGDVGGEADDAEVVRIVGVFVGLVAAEETPAAVVFNKG GFAVEEADGP					
g681	FGLGKQCGGFRVFGDVGGEADDAEVVGVGVFVGFVAAEETPAAVVFNKG GFAVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
g681	VLFGDGVGGDAAVECRGKCLCKVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTGGGTG AAGCGTGCTT GTACGATGCC
201 GATGCGGAGG TGTTCGCCGT CGAGGTTGGG GGCATGGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAACGGG GGCCTTCGCG TAGAGGAAGC CGACGGGCTG GTTTTGTGTT
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGGTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGGAAAC TTGCGGATTT
651 TACCACGATT CTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTGCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  ITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFESSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFNKG GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGKLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFESSATPNSWRVRQQTLSISLPISLV					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFESSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVG DGLECAVFGKLPCAA					
a681	KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVG DGLECAVFCQFPRAA					
	70	80	90	100	110	120



1093

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHYGN	TLGXKLTDFTTIR	ALSADGGGLVVQ	CAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHCGN	TXGGKLADFTTIL	ALSADGGGLVVQ	CAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

**g682.seq**

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

**g682.pep**

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

**m682.seq**

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTTCGA CAAGGCAGTC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

**m682.pep**

```

1  MRDFTVWVS Y GKWKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY... EMAMPSEP DWIQTAFDMA YGFIRFPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

**m682/g682**

1094

	10	20	30	40	50	60
m682.pep	MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC					
	:       :                 :					
g682	MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC					
	10	20	30	40	50	60

  

	70	80	90	100	110
m682.pep	PILILIDY-----EMAMPSEPDWIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR				
		:			
g682	PILILIDYICVNDEIKMPSEPDWIQTAFCMA-GFIRFPTDRPILTRQSGVVRISPRTGFR				
	70	80	90	100	110

  

	120	130
m682.pep	YPTRSLPKSKKAYGX	
g682	YPTRSLPKSKKAYGX	
	120	130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```
a682.seq
1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA
```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```
a682.pep
1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL SSTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIEY.. ..YIRFPTDR
101 PILTRPTGVV RISPRTGFRY PTRSLPKSKK AYG*
```

m682/a682 80.6% identity in 129 aa overlap

	10	20	30	40	50	60
m682.pep	MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC					
a682	MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC					
	10	20	30	40	50	60

  

	70	80	90	100	110	120
m682.pep	PILILIDYEMAMPSEPDWIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS					
	:		:		:	
a682	PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS					
		70	80	90	100	

  

	130
m682.pep	LPKSKKAYGX
a682	LPKSKKAYGX
	110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```
g683.seq
1  ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTACT
51  CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151 GACAGTGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTATTGTA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
```

1095

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >:

**g683.pep**

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK  
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL  
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

**m683.seq..**

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT  
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG  
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA  
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT  
201 TGTTACCAAT CTAAACAAG AACGTTTGC CAACACCCCG GCATACAAGA  
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA  
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA  
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA  
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

**m683.pep..**

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK  
51 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL  
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

**m683/g683** 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMSILSGTLTEKQYETVCGKKLX					
g683	SSLRPMSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

**a683.seq**

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT  
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG  
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA  
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT  
201 TGTTACCAAT CTAAACAAG AACGTTTGC CNACACCCCG GCATACAAGA  
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA  
301 AGTTCGCTAC AATGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA  
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA  
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

**a683.pep**

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK  
51 DSVRKNGNLM IFXDKKVVTN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFXDKKVVTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
a683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACCGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAC	CTTTGTTTCT
301	GCCTCAGCA	GCGGCAGTAC	CGACAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLFPIAAAL	TLAACGTVQS	TOYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRINTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQQM	VE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTTCT
301	GCCTCAGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLFPIAAAL	SLAACGTVQS	TOYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD

151 GYAAMTAALE QGLKQAAQOM VE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

**m684/g684** 97.7% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
g684	MRLFPIAAALTLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTEKWTVYIDAFQGS					
g684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTDKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

**a684.seq**

1	ATGCGCCTCT	TCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

**a684.pep**

1	MRLFPIAAAL	TLAACGTVQS	TQYFVLPDSR	YIRPATQGGE	TAVEVRLAEP
51	LKRGGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSGTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQOM	VE*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

**m684/a684** 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
a684	MRLFPIAAALTLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTEKWTVYIDAFQGS					
a684	DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTEKWTVYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	

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```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
              |||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGCGCGTGG TTTCTGCAGG
51 TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGcct GCGCCGTCTT GCCGGCCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCTGTGCCA CGCTGACCGT GCCGACCGCG CGGGCGGATG
251 CCGTTGTGCC GAAGAATCCC GAACGcgctcg ccgtgtAcga CtggGCGGCG
301 TtggATACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTC AGCCTGCATT TGACAAGGCG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCATTA CCGGCGGGCC GGGTGCAGAA GCGTATGAAC AGTTGGCGAA
501 AAACCGGACC ACCATAGATT TGACGGTGGA CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCTG GGATTTCGG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTCC CCGAAAAGCG
651 CGAAGCCGCC AAAGGCAAG GACGCGGGCT GGTGCTGTCT GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGGCA
801 CCGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAGG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGCGCGG GTTTGAAAAA
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685>:

```

g685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51 CSPEPAEAKT VSAASQAAST PVATLTVPTA RGDVAVPKNP ERVAVYDWAA
101 LDTLLEPGVN VGATTAPVRV DYLPAPFDKA ATVGTLFEPD CESLHRHNPQ
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNNG IRTSGEKQME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAGF TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFEYIKEKN PGWIFIIDRT AAIGQEGPAA
301 VEVLDNALVC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TCGCGCGTGG TTTCTGCAGG
51 TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCTT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGCGCTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCC
401 AGCCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGGGGCGCG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCTGG TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC CGAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCTTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAATT ACATTGTCGC GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGCGGCGCT TTAAGGAGC AGAACCCGTT
1051 GCGGCGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pep

1099

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKKGK RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQ LKAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
              |||||
g685           LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT
              10      20      30      40      50      60

              70      80      90      100     110
m685.pep      VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
              ||||| :| |||||
g685           VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV
              70      80      90      100     110     120

              120     130     140     150     160     170
m685.pep      DYLPAPAFDKAATVGTTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGN
              |||||
g685           DYLPAPAFDKAATVGTTLFEPDCESLHRHNPQFVITGGPGAEAYEQLAKNATTIDLTVDNGN
              130     140     150     160     170     180

              180     190     200     210     220     230
m685.pep      IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSVTGNKVSAGF
              |||||
g685           IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKKGKRGVLVSVTGNKVSAGF
              190     200     210     220     230     240

              240     250     260     270     280     290
m685.pep      TQSRLASWIHGDIGLPPVDESLRNEGHPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
              |||||
g685           TQSRLASWIHGDIGLPPVDESLRNEGHPVSEFYIKEKNPGWIFIIDRTAAIGQEGPAA
              250     260     270     280     290     300

              300     310     320     330     340     350
m685.pep      VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQ LKAAFKKAEPV AAGKKX
              |||||
g685           VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQ LKAAFEKAEPV AAQX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTTGCC GTATCGGGAA TTTTGCCTTT TCGCGCTGG TTTCTGCAGG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAACCC GCGTTTATAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTTGCAG CTTGCATTG ACAAGCGCGC AACGTTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTATTACC
451 GGCGGGCCCG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCGAAAAAG
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGGCGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAAGG CGCGGGCTGG TGCTGTCCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

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```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCCCT GCCGCGAACT ACATTGTGCG GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

**a685.pep**

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSE FYIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQ KEAFKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

**m685/a685** 98.9% identity in 355 aa overlap

	10	20	30	40	50	60
m685.pep	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
a685	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
	10	20	30	40	50	60
m685.pep	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
a685	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
	70	80	90	100	110	120
m685.pep	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
a685	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
	70	80	90	100	110	120
m685.pep	PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
a685	PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
	130	140	150	160	170	180
m685.pep	PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
a685	PAFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
	130	140	150	160	170	180
m685.pep	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGFTQSR					
a685	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGFTQSR					
	190	200	210	220	230	240
m685.pep	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGFTQSR					
a685	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGFTQSR					
	190	200	210	220	230	240
m685.pep	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
a685	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
	250	260	270	280	290	300
m685.pep	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
a685	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
	250	260	270	280	290	300
m685.pep	DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFKKAEPVAAGKKX					
a685	DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQKAAFEKAEPVAAGKEX					
	310	320	330	340	350	
m685.pep	DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFKKAEPVAAGKKX					
a685	DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQKAAFEKAEPVAAGKEX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

**g686.seq (partial)**

```

1  ..AATTTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgcgCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCGTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCGGCAA GCCGTGTGCC GGTGCTGCGG TTGTCGGTCA
201 GGTTAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTG CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```



This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686>:

```
g686.pep (partial)
1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

```
m686.seq..
1  ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCGGCAT TGGTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGC TACGATACT ACCGGCATTG
251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTTCGT TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTC AACG GGACTACCG CTTCATCAGA ATCGGAATGT GA
```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

```
m686.pep
1  MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
51  GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
151 SVNGTTGFIR IGM*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

```

                                     10      20      30
g686.pep                          NFSCRADDVFDDICSAVEGFGGIARSVQLG
                                     |||  ||||:|||||||
m686      LKKFVLGGIAALVLAACGSGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
               10      20      30      40      50      60

               40      50      60      70      80      90
g686.pep      AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
               |||  ||||:|||||||
m686      AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
               70      80      90      100     110     120

               100     110     120     130
g686.pep      GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFVRIGMX
               |||  ||||:|||||||
m686      GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFVRIGMX
               130     140     150     160
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

```
a686.seq (partial)
1  ..AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAAGCTTC GCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
151 ATTGTGGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CCGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

```
a686.pep (partial)
```

1102

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG
51  IVETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101  AVGGMVFVSV PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. meningitidis*:

```

m686/a686    96.2% identity in 131 aa overlap

              10      20      30      40      50      60
m686.pep     LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDFVNDICSAVEGFGGIARSVQLG
a686          ||||| |||||:|||||:|||||
              10      20      30
              70      80      90      100     110     120
m686.pep     AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
a686          ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
              40      50      60      70      80      90
              130     140     150     160
m686.pep     GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFIRIGMX
a686          ||||| |||||:|||||:|||||:|||||
              100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GCGGTGCGG CCTGTTCGC
51  CCTTGCCGGG TCGGACAGCA AAGTCCAAAC CAGCGTCCCC GCCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCCGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTCG GCTATTTTG TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCGC TGGCACGCct
351 cGCCGCCGCC GTGATATGCG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACAa ACcgcttTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCCGAAAG TCAGCGCGGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAATCG ACGGTACGCC CACGGTTATC
601 GTCGGCGGCA AATATAAAGT CGAATTTGCC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGCGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687 >:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGQ
51  NYTVLANPIP QQQAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWVWKE MLPLARLAAA VDMAAAESKD VANSHIFDAM VNQIKIKLQEP
151 EVLKKWLGEQ TAFDGKKVLA AYESPESQAR AGKMQELTET FQIDGTPTVI
201 VGGKYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCGGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACCGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAAGCA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCGGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT

```

```

501 TGCCGCCTAC GAGTCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAGGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QRIKLQNPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687  97.0% identity in 234 aa overlap

          10      20      30      40      50
m687.pep  MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
          |||||  |||||  |||||  |||||  |||||
g687       MKSRHLALALGV AALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
          10      20      30      40      50      60

          60      70      80      90      100     110
m687.pep  QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTHEHVWVQKEMLTLARLAAA
          |||||  |||||  |||||  |||||  |||||  |||||
g687       QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTHEHVWVQKEMPLARLAAA
          70      80      90      100     110     120

          120     130     140     150     160     170
m687.pep  VDMAAADSKDVANSHIFDAMVNQIKLQNPVLEVKWLGEQTAFDGKKVLAAYESPESQAR
          |||||  |||||  |||||  |||||  |||||  |||||
g687       VDMAAAESKDVANSHIFDAMVNQIKLQEPVLEVKWLGEQTAFDGKKVLAAYESPESQAR
          130     140     150     160     170     180

          180     190     200     210     220     230
m687.pep  ADKMQLTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          |||||  |||||  |||||  |||||  |||||  |||||
g687       AGKMQLTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGCGGTT GCCGCCCTGT TCGCACTTGC
51  CGCGTGCAGC AGCAAAGTCC AAACCAGCGT CCCC GCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCG CCGGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCTCTT CCAACCCGAT TCCCAACAG CAGCAGGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCT TCTGGCAGAA AGAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAGGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QRIKLQEPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

m687.pep	10	20	30	40	50	60
	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAAASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
m687.pep	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWQKEMTLARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWQKEMTLARLAAAVD					
	70	80	90	100	110	120
m687.pep	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNEPVLLKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKLQNEPVLLKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
m687.pep	190	200	210	220	230	
	KMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX					
a687	KMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTTGCACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTCGCTGTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTGCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688>:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAAEAL	RAKQNADKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTTGCACAG	AAAGGCATTT	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCACGTGTC	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACTCG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCGC	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCATTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGTCCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

```
m688/g688    90.6% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYP SRFAQKGISVNKTLILALSALLGLAACS AERVSLFSPSYKLKIIQGNELEPRAVAA
              |||  |||||  |||||  |||||  |||||  |||||
g688          VLHXTSRFAQKGSPVNKTLILALSALFSLTACSV ERVSLFSPSYKLKIIQGNELEPRAVAA
              10      20      30      40      50      60

              70      80      90     100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI I KERSNLT VYFENGVLVRTEG
              |||||  |||||  |||||  |||||  |||||  |||||
g688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI I KERSNLT VYFENGVLVRTEG
              70      80      90     100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDKPX
              :|||  |||||  :|||
g688          DALQNAAEALRAKQNA DKQX
              130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATAACGGGC
151 AACGAAC TCG AACCTCGCGC CGTCGCCTCC CTCCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
1  VLHYP SRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLKIIQG
51 NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLT VYF ENGVLVRTEG NALQNAAEAL RVKQNA DKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688    93.5% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYP SRFAQKGISVNKTLILALSALLGLAACS AERVSLFSPSYKLKIIQGNELEPRAVAA
              |||||  |||||  |||||  |||||  |||||  |||||
a688          VLHYP SRFAQKGISVNKTLILALSALLGLAACS VERVSLFSPSYKLKIIQGNELEPRAVAS
              10      20      30      40      50      60

              70      80      90     100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI I KERSNLT VYFENGVLVRTEG
              |||||  |||||  |||||  |||||  |||||  |||||
a688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI I KDRSNLT VYFENGVLVRTEG
              70      80      90     100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDKPX
              :|||  |||||  :|||
a688          NALQNAAEALRVKQNA DKQX
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCTAC CTGCCCCGCA
101  TTCCCGAAAT GGCAGCGCG CTGAACGCGG ATATCCACCG TATCGAATAG
151  AGTCTGAGTT TGTATTATGTT CGGCACGGCG TTCCGGGCAAG TGGCCGGCGG
201  CGCGGTGTCC GACATCAAAG GCGCAAAACC CGTCGCCCTG ACCGGTTTGA
251  TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTGCTTC GAGTACCGAA
301  CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCCGGCGCAG GCATGGCTGT
351  AGTCATCGTC ggtgcgatgg tgcgcgatTA TTATCCGGA CGCAAAGCCG
401  cgcAGATGTT TGCCCTTATC GGCATCATTC TGATGGTTGT GCCGCTGGCC
451  GCACCCATGG TCGGCGCATT GTTGCAAGGA TTGGGCGGAT GCGGGCGCAT
501  TTTCTGTTTC ttggcGgcgT ATTGCGCGGT GCTGCCCGGT TTGGTACAGT
551  ATTTCTTGCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTT
601  GGGCTGGTGG CCGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCCGCAT
651  GGGTtatCTG TTTTTCAGG CATTGAGCTT CGGTTCGATG TTCGCCCTTC
701  TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACTG TACGCCGCAC
751  CGGTACGCAT GGGTGTGTTG ACTCAACATC ATCAGCATGA TGTTTTTCAG
801  CCGCGTTACC GCGTGGCGGC TTAAGACCGG CGCGCATCCG CAAAGCATCC
851  TGCTGCGGGG GATTGTGCTC CAATTGCGC CCAACCCGTC CCAACTCGCC
901  GCCGTGCTGT TTTTCGGGTT GCGCCCGTTT TGGCTGCCGG TCGCGTCCGT
951  GATGTTTTCC GTCGGTACGC AGGGCCTGGT CGGTGCCGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTCG
1051 GGTGTATTCC GGTCCCTAAT CCGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGGAAGGAAA ACGAAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

g689.pep (partial)

```

1  ..SPPLPEMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFHTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101  QLLNLRAVQA FGAGMAVVIV GAMVRDYYSR RKAQMFLAI GIILMVVPLA
151  APMVGALLQG LGGWRAIFVF LAAYSPVLPV LVQYFLPNPA VGGKIGRDVF
201  GLVAGRFRKV LKTRAAMGYL FFQAFSFGSM FAFLETSFV YRQLYHVTPH
251  RYAWVFALNI ITMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSOLA
301  AVLFFGLPPF WLPVACVMFS VGTQGLVGAD TQACFMYSYK EEGGSANAVS
351  GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKRRII

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CCGGGCTTTT
51  GTTGCCGCTT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101  GTGTTTTCGG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151  CCTTCTGCCA ATTATCCTGA AATGAGCGAA AAAGTATGAG CGGTTTGTAT
201  GCGGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251  CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301  CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTTCG
351  CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401  TGATTGTATA TTGCCCTGCC GTTGCCGCCA TCGTATTGTT TTCGAGTGCC
451  GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTGCGTG CCGGCATGAC
501  TGTGGTCATC GTCGGCGCAA TGGTGCAGCA TTATTATTCC GGACGCAAAG
551  CCGCCAGATG GTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601  GTCGCACCCA TGGTCGGGCG ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651  GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701  AGTATTTCTT GCCCAAGCCC GCGTCGGCG GCAAAATCGG ACGGACGCTG
751  TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
801  GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTTC ATGTTGCGCT
851  TTCTGACCGA ATCTTCCTTC GTGTACGAGC AGCTCTACCG TGTTACGCCT
901  CATCAATACG CTTGGGCGTT TGCACCAAC ATCATACGA TGATGTTTTT
951  CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CCGCGTGCAT CCGCAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTC GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGCTGCT TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGCGG
1151 CGTGTGTTAT GTCCTATTTT AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTCTTTCAC GACGGTTCGG CAACCGTGAT GCGGGCAACG ATGACCGCGT
1301 CCACCTCTTG CCGCATTCGC CTCTGTGGC TCTGCTCGCA TCGTGCCTGG

```

1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 2294; ORF 689&gt;:

m689.pep  
 1 LLIHYIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM  
 51 PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE  
 101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLIVYCLA VAAIVFVSSA  
 151 EQLNLNRVQ AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL  
 201 VAPMVGALLQ GLGGWQAI FV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV  
 251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYRVTP  
 301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH PQSILLWGIV VQFAANLSQL  
 351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV  
 401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW  
 451 KENGQSEYL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

m689.pep	30	40	50	60	70	80
	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSIDAY					
g689					SPPLPMSGKLMMAVLMVAVLMPFSIDAY	
				10	20	30
m689.pep	90	100	110	120	130	140
	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV					
g689	LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV					
	40	50	60	70	80	90
m689.pep	150	160	170	180	190	200
	AAIVFVSSAEQLNLNRVQAFGAGMTVVIVGAMVRDYSGRKAAQMFALIGIILMVVPLV					
g689	AAIVFASSTEQLNLNRVQAFGAGMAVVIVGAMVRDYSGRKAAQMFALIGIILMVVPLA					
	100	110	120	130	140	150
m689.pep	210	220	230	240	250	260
	APMVGALLQGLGGWQAI FV FLAAYSLVLLGLVQYFLPKPAVGGKIGRDV FGLVAGRFRKRV					
g689	APMVGALLQGLGGWRAIFVFLAAYSPVLPGLVQYFLPNPAVGGKIGRDV FGLVAGRFRKRV					
	160	170	180	190	200	210
m689.pep	270	280	290	300	310	320
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVTPHRYAWVFALNIITMMFFSRVT					
	220	230	240	250	260	270
m689.pep	330	340	350	360	370	380
	AWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMF SVGTQGLVGAN					
g689	AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMF SVGTQGLVGAD					
	280	290	300	310	320	330
m689.pep	390	400	410	420	430	440
	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689	TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL					
	340	350	360	370	380	
m689.pep	450	460				
	LWLCSHRAWKENGQSEYLX					
g689	LWLCSHKAWKENEKKRIL					
	390	400				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCGG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAAGTATGCG CGGTTTGTAT
201 GGCAGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCACG GCGTTCGGAC AGGTGGTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGTCTA CTGCCTTGCC GTTGCCGCCA TCGTATTTCG TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTGCGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCSCGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTGT TTTCTGGCGG CGTATTGCGT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCCG
801 GATGGGTAT CTGTTTTC AGGCATTCAG CTTGCGTTCG ATGTTGCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAGTACG CTTGGGCGTT TGCACCAAC ATCATCACGA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGCGTT GGTGCGTGCA AACACGCAGG
1151 CGTGTTTTAT GTCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGCAC
1251 CTTCTGTCAC GACGGTTCGG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGCGC TCTGCTCGCA TCGTGCCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1  LLIHYIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVO AFGAGMTVVI VGAMVRDYSY GRKAAQMFAL IGILMVVPL
201 VAPMVGALLQ GLGGWQAIHV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYHVT
301 HOYAWAFALN IITMFEFNRI TAWRLKTGVH PQSILLWGIV VOFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA VGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

	10	20	30	40	50	60
m689.pep	LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
a689	LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
	10	20	30	40	50	60
m689.pep	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
a689	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
	70	80	90	100	110	120
m689.pep	SDIKGRKPVALTGLIVYCLAVAAIVFVSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS					
a689	SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYS					
	130	140	150	160	170	180
m689.pep	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIHVFLAAYSLVLLGLVQYFLPKP					
a689	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIHVFLAAYSLVLLGLVQYFLPKP					
	190	200	210	220	230	240
m689.pep						
a689						



```

|||||
a689  GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYS LVLLGLVQYFLPKP
      190      200      210      220      230      240

      250      260      270      280      290      300
m689.ppep  AVGGKIGRDV FGLVAGRFKRV LKTRAA MGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
      |||||
a689  AVGGKIGRDV FGLVAGRFKRV LKTRAA MGYLFFQAFSFGSMFAFLTESSFVYQQLYHVT
      250      260      270      280      290      300

      310      320      330      340      350      360
m689.ppep  HQYAWAFALNI ITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAV LFFGLPP
      |||||
a689  HQYAWAFALNI ITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAV LFFGLPP
      310      320      330      340      350      360

      370      380      390      400      410      420
m689.ppep  FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGM AATFLH
      |||||
a689  FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGM AATFLH
      370      380      390      400      410      420

      430      440      450      460
m689.ppep  DGSATVMAATMTASTSCGIAL L WLC SHRAWKENGQSEY L X
      |||||
a689  DGSATVMAATMTASTSCGIAL L WLC SHRAWKENGQSEY L X
      430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

g690.seq (partial)

```

1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCCAAAC CGATTGCAA
151 CCGGCGCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCCTGC ACCCGCCGC CGGCATTGGC GATCTCATAC
251 AGCAAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGGCGGCT ATGACAACAT
351 ACAGCGGCTG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACCCGC GgCAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTGAAG TTTCGGCAAC ATctgCctaT
601 TTgaaccggc ACAaacaacGG ACTTggcgGC AATTTCaAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTT ACGAAAATGG CAAAATCAG CGTATTGTCG TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

g690.ppep (partial)

```

1  MKNKTS SLP L WLAAILAAR SPSKEDKKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQAIEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEPPKRAR YFEVSATSAY
201 LNRHNGLGG NFQYIGQLPG YLKMHEGME NQSLFRLSNR ERNPDKPF LD
251 IHFDENGKIT RIVVYEKN IY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

m690.seq.

```

1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGCTGTCTC GTCCTCCGCG TCATCAGCTC CTTCCCAAAC CGATTGCAA
151 CCGACCCGAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

```

1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
  1 MKNKTSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
 51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEPEPKRTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPKPFPLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

m690/g690 89.3% identity in 408 aa overlap

	10	20	30	40	50	60
m690.pep	MKNKTSLLLWLTAIMLTAC	SPSKDDKTKE	VGASAASSA	SSAPSQTDLQ	PTASAPDNVK	
g690	MKNKTSLLPLWLAAILAARSP	KEDDKTKENGASAASSA	SSASSQTDLOPAASAPDNVK			
	10	20	30	40	50	60
	70	80	90	100	110	120
m690.pep	QAESAPPSNCTSLHPATGID	DLMQQIAEHIDSDCLFALSH	HELETRFGLPDGGYDNIQRL			
g690	QAESAPLXNCTGLHPAAGIGD	LIQIAEHIDSDCLFALSH	NELETRFGLPGGYDNIQRL			
	70	80	90	100	110	120
	130	140	150	160	170	180
m690.pep	LFPDIRPEDPDYHQKIILAI	EDLRYGKRTISRQAQNALME	QERRLREATLLLIQGSQETR			
g690	LFPDIRPEDPDYHQKIMLAIE	DLRYGTRTISRQAQDAIME	QERRLREATLMLTQGSQKTR			
	130	140	150	160	170	180
	190	200	210	220	230	240
m690.pep	GQGEPEPKRTRYFEVSATPAY	SSRHNNGLGGNFQYISQLPG	YLKIHGEMLENQSLFRLSNR			
g690	GQGEPEPKRTRYFEVSATPAY	LNRRHNNGLGGNFQYISQLPG	YLKMHGEMLENQSLFRLSNR			
	190	200	210	220	230	240
	250	260	270	279		
m690.pep	ERNPKPFPLDIHFDENGKIT	RIVVYEKNIYFNPNTGRI				
g690	ERNPKPFPLDIHFDENGKIT	RIVVYEKNIY				
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
  1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
 51 GACCGCGTGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTCT GTCCACGGCA TCCGCGCTT CGTCTCCGC GCCCCAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCGC TCAAAATGCA CCGACCTGCA CCGCCGCCAC GGCATTGACG
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCTGTTT GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTTCCCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAAG
451 CGCAGCATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGGCGA GGAGCCGAAA CGCACGCGTT ATTTTGAAGT TTCGGCAACC
601 CCTGCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGCCAA TTGCCCGGCT ATCTGAAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG  
 751 TTTTATAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT  
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep

1 MKNKTSSLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT  
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA  
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQII LAIEDLRYGK  
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRQGQEEP RTRYFEVSAT  
 201 PAYSSRHNNG LGGNFYIYGQ LPGAALKHGE MLENQSLFRL SNRERNPDKP  
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

	10	20	30	40	50	
m690.pep	MKNKTSSLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPS---	QTDLQPTASAPD				
a690	MKNKTSSLLWLTAAMMLTACSPSKEDKTKENGASAASSTASAPQTDLQPAASAPD					
	10	20	30	40	50	60
	60	70	80	90	100	110
m690.pep	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI					
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI					
	70	80	90	100	110	120
	120	130	140	150	160	170
m690.pep	QRLFPDIRPEDPDYHQIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ					
a690	QRLFPDIRPEDPDYHQIILAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m690.pep	ETRGQGEERPRTTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRL					
a690	ETRGQGEERPRTTRYFEVSATPAYSSRHNNGLGGNFQYIGQLPGYLKIHGEMLENQSLFRL					
	190	200	210	220	230	240
	240	250	260	270	279	
m690.pep	SNRERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNTGRIX					
a690	SNRERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNLGRRX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq

1 GTGCCGCTGC CTGCTCCCTG CCGTTTGTCC AAACCTGCCG CCTCTTTTTT  
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA  
 101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGGCTG  
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAT  
 201 GCGGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATCCGAA CACAGCGGCC  
 251 GCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG  
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTGCGGT  
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC  
 401 AGCAGCAAAT GTGGCTTCTC TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep

1 VLPAPPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL  
 51 TQGHNEELRK IRAAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE  
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWS SCLK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GGCGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTTCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTTGGCGT
351 GGACGAATTG GAAATCCAAC ACCGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691    97.2% identity in 144 aa overlap

           10      20      30      40      50      60
m691.pep    VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g691         VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFOPNCDIRRLGLTQSQHNELRK
           10      20      30      40      50      60

           70      80      90     100     110     120
m691.pep    IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNENEARDYVESRYLSGMDFAVDEL
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g691         IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNENEARDYVESRYLSGMDFAVDEL
           70      80      90     100     110     120

           130     140
m691.pep    EIQRFFHILTPQQQMWLSCLKX
           | | | | | | | | | | | | | | | |
g691         EIQRFFHILTPQQQMWLSCLKX
           130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GGCGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTTCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTTGGCGT
351 GGACGAATTG GAAATCCAAC ACCGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

1113

Homology with a predicted ORF from *N. meningitidis*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. meningitidis*:

m691/a691 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPND	FQPNCDIRRLGLTQSQHNELRK				
a691	VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPLND	FQPNCDIRRLGLTQSQHNELRK				
	10	20	30	40	50	60
m691.pep	IRTAFKMAGDRARLKVHSEHSRRRSVVEI	ISSDVFNREARDYVESRYLSGMDFAVDEL				
a691	IRAAFKMAGDRARLKVHSEHSRRRSVVEI	ISSDVFNREARDYVESRYLSGMDFAVDEL				
	70	80	90	100	110	120
m691.pep	IRTAFKMAGDRARLKVHSEHSRRRSVVEI	ISSDVFNREARDYVESRYLSGMDFAVDEL				
a691	IRAAFKMAGDRARLKVHSEHSRRRSVVEI	ISSDVFNREARDYVESRYLSGMDFAVDEL				
	70	80	90	100	110	120
m691.pep	EIQHRFFHILTPQQQMWLSSCLKX					
a691	EIQHRFFHILTPQQQMWLSSCLKX					
	130	140				
m691.pep	EIQHRFFHILTPQQQMWLSSCLKX					
a691	EIQHRFFHILTPQQQMWLSSCLKX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

g692.seq

1	GTATCGCACA	CACGCTGTCG	CTGTTCGGAA	TCGAtacGCC	GGATTGCGC
51	GAATGGCAGG	GAATGGCGGA	TTAAAGGACA	AAAATGCCGT	CTGAACACGG
101	ATGCGGTTC	GACGGCATCA	TTTATACGA	CTGCCTTATT	TGGCTGCGCC
151	TTCATTCCAT	GCGGCAGGGT	ATTGTAGCC	CTCGAAGCGT	TTGTGCGCGT
201	AGGCTTTGAA	CGCGTCGGAG	TTATAGGCCT	CGGTTACGTC	TTTAAGCCAT
251	TGGCTGTCTT	TGTCGGCGGT	TTTgacGGCA	GACCAAGTTGA	CATAGGCAAA
301	GCTCGGCTCT	TGGAACAGGG	CTTCGGTCAG	CTTCATGCCG	CTGCTTATGG
351	CGTAGTTGCC	GTTGACGACG	GCAAAATCCA	CGTCGGCGCG	GCTGCGCGGC
401	AGTTGTGCGG	CTTCAAGCTC	GACGATTTTG	ATGTTTTTCA	GGTTTTCCGC
451	GATGTCGGCT	TTGGATGCGG	TCAGCGGATT	GATGCCGTCT	TTGAGTTTGA
501	TCCAACCCAG	TTCGTTCCAGC	ATCACCAAGG	CGCGTGCGAA	GTTGGAcggG
551	TcgtTGGGCG	CGGATACGGT	GCTGCCGTCT	TTGACTTCTT	CCAGCGATTT
601	CAGTTTGCCC	GGATACAGTC	CCAAAGGCGC	GGTCGGCACT	TGGAAGGCTT
651	CGGTGATGTC	CAGGTTGTGT	TCTTTTTTGA	AATCGTCAAG	ATAGGGTTTG
701	TGTTGGAAGA	CGTTGATGTC	CAACTCGCCC	TCCGCCAATG	CCAGATTCGG
751	GCGCACATAG	TCggTAAATT	cgaccaatTT	gacgGTGTAg	cTTTTTTTCT
801	CCAGCTCGgc	tTGGATTGTG	TCTTTGACCA	TATcgccgaa	gtcgccacg
851	gTCGTGCCGA	agacgaTTTC	TTTTTTCGCC	GcgccGTTAT	CGGCAGAAGG
901	GGCGGCGgca	gaggctgcGG	GCGCGCTGTC	TTTTtgaccG	ccgCAGGCTG
951	CGAGGATGAG	CGCGAGtgcg	gcggcgga	ggGTTTTGAA	GAAGGTTTTc
1001	atATTTTCTc	ctga			

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692 >:

g692.pep

1	VSHTRCRCSE	SIRRIWRNGR	EWRIKQKCR	LNTDAVQTAS	FYTTALFGCA
51	FIPCGRVFVA	LEAFVRVGFE	RVGVIGLGYV	FKPLAVFVGG	FDGRFPVDIGK
101	ARLLEQGFQ	LHAAAYGVVA	VDDGKIHVGA	AARQLCGFKL	DDFDVFQVFR
151	DVGFGCGQRI	DAVFEDPTQ	FVQHHQGACE	VGRVVGRGYG	AAVFDFQRF
201	QFARIQSQR	GRHLEGFDV	QVVFEEIVK	IGFVLEDVDV	QLALRQCQIR
251	AHIVGKFDQF	DGVAFFLQLG	LDLFFDHIAE	VAHGRAEDDF	FFRRAVIGRR
301	GGGRGCGRAV	FLTAAGCEDE	RECGGKGFE	EGFHIFS*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

m692.seq

1	GTGTTGCACA	CGCTTTGTCG	CTGTTCGGAA	TCGATACGCC	GGATTGCGCG
51	GAATGGCAGG	GAATGGCGGA	TTAAAGGACA	AAAATGCCGT	CTGAACACGG
101	ATACAGTTCA	GACGGCATCA	TTTATACGA	CTGCCTTATT	TGGCTGCGCC
151	TTCATTCCAT	GCGGCAGGGG	ATTGTAGCC	CTCGAAGCGT	TTGTGCGCGT
201	AGGCTTTGAA	CGCGTCGGAG	TTATAGGCCT	CGGTTACGTC	TTTAAGCCAT
251	TGGCTGTCTT	TGTCGGCGGT	TTTgacGGCA	GACCAAGTTGA	CATAGGCAAA
301	GCTCGGTTCT	TGGAACAGGG	CTTCGGTCAG	CTTCATGCCG	CTGCTTATGG
351	CGTAGTTGCC	GTTGACGACG	GCAAAATCCA	CGTCGGCGCG	GCTACGCGGC

1114

```

401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCCTCGGC
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGCGG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCCGCACT TGGAAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGC TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTGTG CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTGTCTT TTAGCCGCCG CAGGCGGCGA
951 GGATGAGCGC GAGTGGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1 VLHTLCRCSE SIRRIRRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF E RVGVIGLVY FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFGVLG
151 DVRFQGGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGGRYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVG
301 RSGCGGRAVF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

```

m692/g692 91.1% identity in 338 aa overlap

m692.pep      10      20      30      40      50      60
VLHTLCRCSE SIRRIRRNGREWRIKGQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA
g692          10      20      30      40      50      60
VSHTRCRCSE SIRRIWRNGREWRIKGQKRLNTDAVQTASFYTTALFGCAFI PCGRVFVA

m692.pep      70      80      90      100     110     120
LEAFVRVGFER VGVIGLVYFKPLAVFVGGFDGRPV DIGKARFLEQGFQQLHAAAYGVVA
g692          70      80      90      100     110     120
LEAFVRVGFER VGVIGLVYFKPLAVFVGGFDGRPV DIGKARLLEQGFQQLHAAAYGVVA

m692.pep      130     140     150     160     170     180
VDDGKIHVGA ATRQLRGFKLDDFDVFGVLDVRFQGGQRI DAVFEFDPTQFVEHHQDAGE
g692          130     140     150     160     170     180
VDDGKIHVGA AARQLCGFKLDDFDVFGVLDVRFQGGQRI DAVFEFDPTQFVQHHQGACE

m692.pep      190     200     210     220     230     240
VGRVVGGRYG AAVDFDFQRFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
g692          190     200     210     220     230     240
VGRVVGGRYG AAVDFDFQRFQFARIQSQRGRHLEGFQVVFVEIVKIGFVLEDVDV

m692.pep      250     260     270     280     290
QLALSQCQIR AYIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDFFRRAVVG--
g692          250     260     270     280     290
QLALRQCQIR AHIVGKFDQFDGVAFFLQLGLDLFFDHIAE VAHGRAEDDFFRRAVIGRR

m692.pep      300     310     320     330
GGRSGCGGRA VFLTAAGGEDERECGGGKGFEFGFHIFSX
g692          300     310     320     330
GGGRGCG-RA VFLTAAGCEDERECGGGKGFEFGFHIFSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

a692.seq
1 GTGTTGCACA CGCTTTGTCG CTGTTGCGAA TCGATACGCC GGATTCGGCG

```

1115

```

51  GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTTCGGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTCGA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAAGA CGCGGCGCAA GTTGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAGGCGC GGTCGGCACT TGGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTGTGA AGTCGTCAAG ATAGGGTTTG
701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAAGTT GACGGTGTAG CCTTTTCTT
801 CCAGCTCGGG TTGATTTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCGGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTTT TTGACCGCCG CAGGCGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

**a692.pep**

```

1  VLHTLCRCSE SIRRIIRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGFV RVGVIGLGYV FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFGCGQRI DAVFEFDPQ FVEHHQDAGE VGRVVRGGRG AAVFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDDVD QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

**m692/a692** 98.8% identity in 336 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIIRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
a692	VLHTLCRCSE	SIRRIIRNGR	EWRIKGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m692.pep	LEAFVRVGF	ERVGVIGLGYV	FKPLAVFVGG	FDGRPVDIG	KARFLEQGF	QQLHAAAYGVVA
a692	LEAFVRVGF	ERVGVIGLGYV	FKPLAVFVGG	FDGRPVDIG	KARFLEQGF	QQLHAAAYGVVA
	70	80	90	100	110	120
	130	140	150	160	170	180
m692.pep	VDDGKIHVGA	AATRQLRGFKL	DDFVDFVQV	LDVRFGCGQR	IDAVFEFDP	TQFVEHHQDAGE
a692	VDDGKIHVGA	AATRQLRGFKL	DDFVDFVQV	LDVRFGCGQR	IDAVFEFDP	TQFVEHHQDAGE
	130	140	150	160	170	180
	190	200	210	220	230	240
m692.pep	VGRVVRGGR	GYGAAVDFD	FFQRFQLAR	VQSQRGRH	LEDFGDVQ	IVFFFEVVKIGFVLEDDVDV
a692	VGRVVRGGR	GYGAAVDFD	FFQRFQLAR	VQSQRGRH	LEDFGDVQ	IVFFFEVVKIGFVLEDDVDV
	190	200	210	220	230	240
	250	260	270	280	290	300
m692.pep	QLALSQCQIR	AYIVGKLDQ	FDGVAFFL	QLGLDLFF	DHIAEVAD	GRAEDDFFFRRAVVG
a692	QLALSQCQIR	AYIVGKLDQ	FDGVAFFL	QLGLDLFF	DHIAEVAD	GRAEDDFFFRRAVVG
	250	260	270	280	290	300
	310	320	330			
m692.pep	RSGCGGRAIF	LTAAGGEDER	ECGGKGFE	EGFHIFS		
a692	RSGCGGRAIF	LTAAGGEDER	ECGGKGFE	EGFHIFS		

310 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```

g694.seq
1   TCGGCATTTG TGTTGCCCAA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGTTGCCAA TACTTCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTGACGGCG
401 GTTTCGGGT TGTCGTGCG ATAGCAGATG TCTTCCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGCG GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CCGTGCAAGC TGCCCCATCG TGCCCTTCGAC CTGCGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTCACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTCG TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAAACCGCG
751 CTCCGCCGCT TCCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
801 CCAGTGTGCG GCCCGCGCGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CCTTTTTTCG CGAGTTGTG CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATTCTTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCC ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCATTC CGTGTTTCTG CCGCATTCAC
1051 GTTTTTTTGC TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

```

g694.pep (partial)
1   SAFVLPHKPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPFAGH
51  FMPPSAYGCQ YFPHQHFGRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHQR ASRIKYPETA
251 LRRFLHLRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQV V HDEFVVDVDFV
301 AHINRRAEFF QSTFDNTDCP IHTGAEAARI GKDDGFSVHK FCIPCSDGIH
351 VFLLXLCDGR YCQAPPTPHR RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```

m694.seq
1   TTGGTTTTCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCa
51  GACGGCATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGcAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCTGCGCG TTACGCCGAC TTTGTTTTCG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCGTGCGA TAGCAGATAT CTTCTTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTCT GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAAG CATTTTGCCC GCGCGAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCGCGGGG CAAGTCGCAT CAAACACGCG GAAACCGCGc TCCGCCGCTT
801 CTTGCCGCGC CGCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTCGCG
851 CCGCGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTGTGTC ACGACGAATT TGTTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACCAg CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTCTC
1051 GTTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTTCCAAC ACCGCCAACA CCGCACCgAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```

m694.pep
1   LVSASGTRQK CRLKPVQTAf VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVfALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNHDVALF CQLFDGGLPV

```



```

151  GRIADIIFLV  RIADIGETRV  QRGDDVFGFI  DRERGLADIG  EFVGVSDFEF
201  HSRIDRFQIK  HFARKKLPHR  SFDLDVPLMP  DHDDFTVLGI  QSGDFLMHFR
251  HQRASRIKHA  ETALRRFLPH  RLRYAVCRIN  QCRARRHRFR  VFKNHRTFFT
301  QVVHDEFVFN  DFWAHINRRA  ELFQSTDFTN  DCPHTSAEA  ARIGKDDGFL
351  VHKPGISFSD  GINIFLLGFY  GGRCCPTPT  PHRRR*

```

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

[illegible]

a694.seq					
1	TTGGTTTCCG	ATCCGGCAC	ACGGCAAAAA	TGCCGTCTGA	AGCCTGTTC
51	GACGCGATT	GTGTTGCCA	AACATTCAAC	GCGTGCCTA	ACGTTTGCAC
101	AAATCGGGTT	TGGTTTCGCC	CTCGCGGCGC	AACTCTTTGG	GCAGGACGAA
151	CACAACTGCT	TCTTCCGCAC	CCTCGCCTTC	CGGTACGGTT	TCGTCGCCCC
201	ATCCGCGTAT	GGTTGCCAGT	ACTTCCCGCA	CCAACACTTC	GGCGCGGCAC
251	GCGCCTGCCG	TTACGCCGAC	TTTGTTTTTG	CCCTCAAACC	ATGCGCGTTG
301	CAGGTAGCCT	GCAATTATCA	CCATATACGC	ATGCATTCGG	CGCGATCCCG
351	CCACTTTCGC	CAAGCGGTTG	CTGTGGACG	AATTGGGGCA	ACCGACACA
401	ATCGCATGT	CGCACTGTT	TGCCAACTCT	TTGACGGCGG	TTTGCCGGTT
451	GTCGTCGCA	TAGCAGATAT	CTTCTCTGTG	CGGATTCGGG	ATATTGGGGA
501	AACGCGCGTT	CAGCGCGGCG	ATGATGTCTT	TGTTTTCATC	ACCGGACGAC
551	GTGGTTTGGC	TGACATAGGC	GAGTTTGTGC	GGGTTTCTGA	CTTCGAGTTT
601	TGCCACATCT	CCGACCGTTT	TCGACAAAAG	CATTTTGCCC	GATCGAAGCT
651	GCCCCATCT	TCCTTCGACC	TCGACGTGCC	CCTTATGCCC	GGCCATGATG

1118

```

701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTGTGTC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTCTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 QVTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

**a694.pep**

```

1  LVSASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRVAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

**m694/a694** 100.0% identity in 385 aa overlap

	10	20	30	40	50	60
m694.pep	LVSASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
a694	LVSASGTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m694.pep	AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL QVACIIHHIR IDSARCRHFA					
a694	AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL QVACIIHHIR IDSARCRHFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m694.pep	QAVAVGRIGR TDHNDHVALFCQLFDGGLPV GRRADIIFLV RIADIGETRV QRGDDVFGFI					
a694	QAVAVGRIGR TDHNDHVALFCQLFDGGLPV GRRADIIFLV RIADIGETRV QRGDDVFGFI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m694.pep	DRERGLADIG EFVGVSDFEF CHISDRFDQKH FARRKLPHRSFDLDVPLMP DHDDFTVLGI					
a694	DRERGLADIG EFVGVSDFEF CHISDRFDQKH FARRKLPHRSFDLDVPLMP DHDDFTVLGI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m694.pep	QSGDFLMHFR HQRASRIKHA ETALRRFLPH RLRVAVCRIN QCRARRHFRQ VFNKHRTFFT					
a694	QSGDFLMHFR HQRASRIKHA ETALRRFLPH RLRVAVCRIN QCRARRHFRQ VFNKHRTFFT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m694.pep	QVVHDEFVNV DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL VHKPGISFSD					
a694	QVVHDEFVNV DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL VHKPGISFSD					
	310	320	330	340	350	360
	370	380				
m694.pep	GINIFLLGFY GGRCCPTPPT PHRRRX					
a694	GINIFLLGFY GGRCCPTPPT PHRRRX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1  TTGCTCAAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTGACCCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCTG
251 CCTCTGTGC TTCCGTTTTC CCGTTCCGG AGGCGAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTGCAACG
401 AAGTGGAAT GTTAAACGGG AAAGTCAAAG CATGGAGCA TACGAAAATA
451 CACCCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACTA TCAAAACGGC
601 AGGTTTCTG CCGCAGCCGC CTGTGTAAG GGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```
g695.pep
1  LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCNSQRF QSKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGSRTM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRITYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMNCES VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1  TTGCTCAAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGCTG TCTGTGTCCG
251 CTTCTGTGC TTCCGTTTCA CCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGAAGGCAA AATCGTCCGG CTGTGCAACG
401 AAGTGGAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACTA TAAAAGCGGC
601 AAGTTTCTG CCGCTGCCTC CTTGTGAAA GCGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1  LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYKSG
201 KFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMNCES VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

	10	20	30	40	50	60
m695.pep	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
	:     :			:		
g695	LPQTRPARRHHRQYFVERKGDARSGFXCAAQCNSQRFQSKPAERYADCPHHPARRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m695.pep	LDPASEKIMKIKLPLFIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
	:					
g695	FDPASEKIMKTKLPLFIWLSVSASCASVLPVPEGSRTemptQENASDGIPYPVPTLQDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m695.pep	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLLDRKLKEHYLNTEGGSASA					
g695	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLLDRKLKEHYLNTEGGSASA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m695.pep	HTVETAQNLNQALKHYKSGKFSAAASLLKGADGGDGGGSAQRSMYLLQLSRARMGNCS					
g695	HTVETAQNLNQALKHYQNGRFSAAAALLKGADGGDGGGSAQRSMYLLQLSRARMGNCS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m695.pep	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
g695	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
	250	260	270	280	290	300
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

1	TTGCCTCAAG	CTTGTCGGGC	AAGGCGGCAT	CATTGCCATC	GACAATATTT
51	TGTTGAACGG	AAGGGTGATG	CGCGAAGCGG	CTTCCGATGC	GCCGCCAGC
101	GTCGGCATCC	TCAAAGATTT	TAATCAAAC	CTGCCGAACG	ATACGCGGAT
151	TGTCCCATC	ACCCTGCCCG	TCGGCGACGG	TTTGACCTG	CTTCTGAAA
201	AATAATGAAG	ACCAAATAC	CGCTTTTAT	CATTTGGCTG	TCCGTATCCG
251	CCGCCTGTT	TTCCCTGTT	TCCGCAATA	TTCAGGATAT	CGCGCTCGAA
301	CCGCAGGCAG	AGGCAGGTAG	TTCGGACGCT	ATTCCCTATC	CCGTTCCAC
351	TCTGCAAGAC	CGTTTGATT	ATCTGGAAGG	CACACTCGTC	CGCTGTGCA
401	ACGAAGTGGA	AACCTTAAAC	GGCAAAGTCA	AAGCACTGGA	GCATGCGAAA
451	ACACACCTT	CCAGCAGGGC	ATACGTCCAA	AAACTCGACG	ACCGCAAGTT
501	GAAAGAGCAT	TACCTCAATA	CCGAAGGCGG	CAGCGCATCC	GCACATACCG
551	TCGAAACCGC	ACAAAACCTC	TACAATCAGG	CACTCAAACA	CTATAAAAGC
601	GGCAGGTTT	CTGCCGCTGC	CTCCCTGTTG	AAAGGCGCGG	ACGGAGGCGA
651	CGGCGGCAGC	ATCGCGCAAC	GCAGTATGTA	CCTGTTGCTG	CAAAGCAGGG
701	CGCGTATGGG	CAACTGCGAA	TCCGTCATCG	AAATCGGAGG	GCGTTACGCC
751	AACCGTTTCA	AAGACAGCCC	AACCGCGCCT	GAAGCCATGT	TCAAAATCGG
801	CGAATGCCAA	TACAGGCTTC	AGCAAAAAGA	CATTGCAAGG	GCGACTTGGC
851	GCAGCCTGAT	ACAGACCTAT	CCCGGCAGCC	CGCGGCAGAA	ACGCGCCGCC
901	GCAGCCGTGC	GCAAACGATA	G		

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

1	LPQACPARRH	HCHRQYFVER	KGDARSGFRC	AAQRRHPQRF	*SKPAERYAD
51	CPHHPARRRR	FDPASEKIMK	TKLPLFIWL	SVSAACSSPV	SRNIQDMRLE
101	POAEAGSSDA	IPYPVPTLQD	RLDYLEGLTV	RLSNEVETLN	GKVKALEHAK
151	THPSSRAYVQ	KLDDRKLKEH	YLNTEGGSAS	AHTVETAQNL	YNQALKHYKS
201	GRFSAAASLL	KGADGGDGGG	IAQRSMYLLL	QSRARMGNCE	SVIEIGGRYA
251	NRFKDSPTAP	EAMFKIGECQ	YRLQKDIAR	ATWRSLIQTY	PGSPAAKRAA
301	AAVRKR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

m695.pep	10	20	30	40	50	60
	LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAPHRPHHPARRRR					
a695	10	20	30	40	50	60
	LPQACPARRHCHRQYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR					
m695.pep	70	80	90	100	110	
	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQT--EMSTRENASDGIPYPVPTL					
a695	70	80	90	100	110	
	FDPASEKIMKTKLPLFIIWLSVSAACSS--PVSRIQDMRLEPQAEAGSSDAIPYPVPTL					
m695.pep	120	130	140	150	160	170
	QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGS					
a695	120	130	140	150	160	170
	QDRLDYLEGTIVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTEGGS					
m695.pep	180	190	200	210	220	230
	ASAHTVETAQONLYNQALKHYKSGKFSAAASLLKGADGGDGGGIAQRSMYLLQLSRARMGN					
a695	180	190	200	210	220	230
	ASAHTVETAQONLYNQALKHYKSGRFSAAASLLKGADGGDGGGIAQRSMYLLQLSRARMGN					
m695.pep	240	250	260	270	280	290
	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRS LIQTYPGSPA AKR					
a695	240	250	260	270	280	290
	CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRS LIQTYPGSPA AKR					
m695.pep	300					
	AAAAVRKRXX					
a695	300					
	AAAAVRKRXX					

The following partial DNA sequence was identified in *N. gonorrhoeae*

g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:

g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

m696.seq

1	TTGGGTGCC	GGCAGGCGGC	ATCCCATCAT	TTTGCCAAG	GCAACAAATT
51	ATTTGGCGGC	ATCTTTCATT	TTGTCTGCCG	CTTCCTGAGT	CGCGTCGGCA
101	GCTTTGTTC	AAGTATCTTT	AGCTGCTTCA	GTTACAGCTT	CTTTGGCTTC
151	AGTTACAGCT	TCCTCGGCAC	TTGCCTTTGC	ATCAGCCGCA	GCATCTTTGA
201	CTTGGTCTTT	CGCTTCTTCG	ACGGCAGAAAG	CGGCAGACTC	GGCGGCAGAA
251	GCCGCAGTGT	CTTTAACATC	GGA CTCAACG	GCTTGAACCG	CTTCCTTAAC
301	CTCCTGTTTG	GCTTCTTGCG	AACAAGCTGC	CAAGGCAGCC	GCCATCATTG
351	CGGCAATCAA	TAA			

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

m696.pep

1	LGCRAASHH	FCQGNKLFGG	IFHFVCRFLS	RVGSFVQSIF	SCFSYSFFGF
51	SYSFLGTCLC	ISRSIFDLVF	RFFDGRSGRL	GGRSRSVFNI	GLNGLNRFLN
101	LLFGFLRTSC	QGRHHCNGQ	*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:

a696.seq

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```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGCTGCGCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GCGGCGAGAA
251 GCCGCAAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTGGC AACAAGCTGC CAAGGCAGCC GCCATCATG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1   LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSEFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRVFN IGLNGLNRFLN
101 LLFGFLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696    100.0% identity in 120 aa overlap

          10      20      30      40      50      60
m696.pep    LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
a696         LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
          10      20      30      40      50      60

          70      80      90     100     110     120
m696.pep    ISRSIFDLVFRFFDGRSGRLGGRSRVFNIGLNGLNRFLNLLFGFLRTSCQGSRRHHCGNQ
a696         ISRSIFDLVFRFFDGRSGRLGGRSRVFNIGLNGLNRFLNLLFGFLRTSCQGSRRHHCGNQ
          70      80      90     100     110     120

m696.pep    X
            |
a696         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCTA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTFTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACGGCG GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GCGTTGCGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGGTTC GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1   MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSLS
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKGKGVs
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMPS ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

1123

201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA  
 251 VGVGGATSMD FTLPIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSTLG  
 301 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

**m700.seq**

1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG  
 51 ATTTTATATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC  
 101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG  
 151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGAC GATATGGCGT TGACGGTTCT  
 201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT  
 251 TGGGAAAGTT ATTCCTGCGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG  
 301 GTCGGCGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT  
 351 TGCATTCGGC AAACGTATGC GCGATATTG GATGCCGTCT GAAAGCGCGG  
 401 GCATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA  
 451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG  
 501 GTTGTGCGTC TGTTTATGCT TTTTATCTCT TTCGGGCGGG CTGCTGTTTG  
 551 CCGCATCGAC AGACGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC  
 601 GGCTTCGGTT GGTATTCCTT CTCGGGTTTG GTCATGACCG AGGCTTACGG  
 651 CGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT  
 701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTTC AGATGCGGCG  
 751 GTGGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA  
 801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG  
 851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTCCT CGCTTTGGGT  
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

**m700.pep**

1 MD~~SL~~MTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL  
 51 RVEDLGSRLD DMALT~~VL~~WLF VCTVGANLLA LAVLGKLFPP RIKGKGVSV  
 101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMPES ESAGMYCLML LVFLIGVQLK  
 151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASTDGV SWTKGLAMAS  
 201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA  
 251 VGVGGATSMD FTLPIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSA  
 301 \*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

**m700/g700**

	10	20	30	40	50	60
m700.pep	MD <del>SL</del> MTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALT <del>VL</del> WLFVCTVGANLLALAVLGKLFPPRIKGKGVSVGVSGSVGQLGCVLLGFAFG					
g700	DMALT <del>VL</del> WLFVCTVGANLLALAVLGKLSPPWRIGGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIQGAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFTLPIQGAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1   ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTCGCCGG
51  ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTGTGCG
151 CGCGTGGAGG ATTTGGGTTT CCGGTTGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAAGTATGAT GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTTG GTCAACCGCA GGGGTATTCT
501 GTTGTGCGTC TGGTTTATGC TTTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCTT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTTGGCA CGAGAGCTGT
701 TCGCGCTGGC ATTTATTCCG CTGCTGATGA AGCGTTTCC CGATGCGGCA
751 GTGGGGGTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCT
801 GGGTGCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTCCT CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1   MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSLS
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPW RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYSLSL VMTEAYGAVW GSIALNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF TLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180



g701.seq

1	ATGTCTTGGC	ACATATTCCA	AGTTGCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGTCTTCGC	CGACGATGGC	GAAAAC TTGT	TTGGAGACGT
101	CGCCGGAAGC	GGGGCTGATG	GTATGGGTCTG	CGCCCAACTC	TTTCGCCGGT
151	TTCAAACGGT	TTTCGTCCAT	ATCGCACACG	ATAATGGCGG	CAGGGCTATA
201	CAGTTGGGCG	GTCACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCGA
251	TGAATACGGT	ATCGCCGGGT	TTCACATCGC	CGTATTGCAC	GCCGATTTTCG
301	TGGGCGGTCTG	GTAAGCGCTC	GCTCAACAGC	AGGGCGCATTT	CTTCGTTGAC
351	GTTGTCTGTC	GGCGGCACGA	GGCTGTTGTC	GGCATAA	

g701.pap

1 MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG  
51 FKRFSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS  
101 WAVGKASLNS RAISSLTLSC GGTRLLSA\*

**m701.seq**

1	ATGTCTTGGC	ACATATTCCA	TGTAGCAGGG	ATACCGACGG	CTTCGATGGC
51	GCAATCCACG	CCGTCTTCGC	CGACGATGCG	AAAGACTTGT	TTGGATACTT
101	CGCCGGAAGC	AGGGTTAATG	GTATGGGTGC	CACCCAATTG	TTTCGCCAGT
151	TTCAAACGGT	TTTCGTTCAT	ATCGCAAACG	ATGATGGCGG	CGGGACTGTA
201	CAGTTGGGCG	GTCAACAGGG	CGGACATACC	GACAGGGCCT	GCCCCAGCGA
251	TGAATACGGT	GTGCGCGGGT	TTGACATCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGGTTCG	GCAAAGCGTC	GCTCAACAAC	AGGGCGAATT	CTTCGTTGAC
351	ATTATCGGGC	AGCGCAACGA	GGCTGTTGTC	GGCATAA	

m701.ppt

1	MSWHIFHVAG	IPASMAQST	PSSPTMAKTC	LDSPEAGLM	VWVAPNSFAS
51	FKRESSISQT	MMAAGLYSWA	VNRADIPTGP	APAMNTVSPG	LTSPYCTPIS
101	WAVGKASLNN	RAISSLTSLG	SGTRLLSA*		

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQT					
	:     :     :     :     :     :     :     :     :     :					
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTCLETSPEAGLMVWVAPNSFAGFKRESSISHT					

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	:     :     :     :     :     :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSC					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
	:					
g701	GGTRLLSAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTG CGCCCAACTC TTTCCGCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTTCG
301 TGTGCGGTTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTCTGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLTG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASF					
	:     :     :     :     :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISLTLSG					
	:     :     :     :     :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLTG					
	70	80	90	100	110	120
	129					
m701.pep	SGTRLLSAX					
a701	SGTRLLSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGTt ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTGAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAAC TGCCCGGCGGT
351 CAGGATTTTCG cgggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

```

1  MPCSKASWTS PGVATPGIRG MPLLRPALAR DSCKPGLMAK TAPASSTALS
51  CSQLVTVPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

**m702.seq**

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

**m702.pep**

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSQLVTVPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

**m702/g702**

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALAR DSCSPGLMAK TAPASSTALS CSQLVTVPAP					
	:					
g702	MPCSKASWTS PGVATPGIRGMPLLRPALARDSCKPGLMAK TAPASSTALS CSQLVTVPAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSIAIRRMASRPTGVRVISRVGMPPSTRAWDKSMAVLKSSIAIT GTTAPAVKIS					
	:					
g702	MMALGISLAIRRMASPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAIT GTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVL RVEWGILLRW DRLX					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

**a702.seq**

```

1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACG CGCCGGCGGT
351 CAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

**a702.pep**

```

1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSQLVTVPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

1128

```

m702.pep      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702          MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
               10      20      30      40      50      60

               70      80      90      100     110     120
m702.pep      TMLAGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702          TMLAGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
               70      80      90      100     110     120

               130     140
m702.pep      RGVSLDISVLRVEWGILLRWDR LX
               |||||||||||||||||||||||||||
a702          RGVSLDISVLRVEWGILLRWDR LX
               130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

**g703.seq**

```

1   ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CCGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATAAAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAACAA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTctgTgc gcTGTtggtt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

**g703.pep**

```

1   MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTRKTGAP
201 DGYVPLKDLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
251 KVPSFDEMKG QIAGNLQAER IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

**m703.seq**

```

1   ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CCGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAACAA ATATTCCCTC AACGACCGTA CCAAACAGAC CCGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGCA ACGCCGCTGA

```

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

**m703.pep**

```

1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV
251 KVPSEFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

```

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

**m703/g703**

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVVNTVVAAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVVNTVVAAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDKEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDKEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSDREVKVPSEFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYYVNSDREVKVPSEFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

**a703.seq**

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAGAAC AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

1130

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

```

a703.pep
  1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDLE QGVPPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDREVS
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703    100.0% identity in 288 aa overlap

      10      20      30      40      50      60
m703.pep    MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
a703         MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
      10      20      30      40      50      60

      70      80      90     100     110     120
m703.pep    LENEVVNTVVAAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
a703         LENEVVNTVVAAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
      70      80      90     100     110     120

      130     140     150     160     170     180
m703.pep    EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG
a703         EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG
      130     140     150     160     170     180

      190     200     210     220     230     240
m703.pep    FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG
a703         FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG
      190     200     210     220     230     240

      250     260     270     280     289
m703.pep    VYYVNDREVSQVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
a703         VYYVNDREVSQVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

```

a704.seq
  1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCAAGAAAT
201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
251 TGGAACCCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
401 TCTGGGACGA CGGCAAAATC CGCCTTTCGG ACATTCTGTT GAAAATCAGG
451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
551 TGGGGATGAT GCAGACGATG ATGTTTCGCG TGCCGACCTA CCTTTACGGC
601 GGCACATCGA AATCCGATTT CCTGCAAATC CTCCATTGGG GCGGCTTTTT
651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

```

1131

```

801  TGC GGGG CAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTC
851  TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901  GCCGCCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTGGCC ATCATATGCC
951  CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGGGC
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCTGC GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGTTCTA
1451 CCGGTACGCT GCGCGCGGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCTCG CCCAAACAC CGACATCAT TTCGACAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTCAG ACGGCAGCGT
1701 CCCCACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGCGCG
1851 CGGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCG CCGTTTGGC
2151 GCAGGCAGAC GTATCCGCCG CCGCAGCGGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1  MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAQS IIDAGLSYY
51  KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QQLLRTDGIV RIDLNYSTHR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMMQTM MFALPTYLYG
201 GDIEPDLFI LHWGGFLMVL PVVFYCAVPF YQALRLDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAELAEQYAS SFIFGELLTA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSQSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRONLIWAG AYNIIAVPLA VLGYPQPWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep  MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVAQSIIDAGLSYYKQRTADAQKT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a704      MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVAQSIIDAGLSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep  ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRTDGIV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLLRTDGIV

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	70	80	90	100	110	120
	130	140	150	160	170	180
m704.pep	RIDLNYSTHRCRVVDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA				
a704	RIDLNYSTHRCRVVDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA				
	130	140	150	160	170	180
	190	200	210	220	230	240
m704.pep	VAGLGMMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVL	PPVVFYCAVPFYQGALRDLKN			
a704	VAGLGMMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVL	PPVVFYCAVPFYQGALRDLKN			
	190	200	210	220	230	240
	250	260	270	280	290	300
m704.pep	RRVGM	DTPI	TVAI	IMT	FIAGV	SLATNAGQGM
a704	RRVGM	DTPI	TVAI	IMT	FIAGV	SLATNAGQGM
	250	260	270	280	290	300
	310	320	330	340	350	360
m704.pep	AAERLVKLI	PAFCHHMPDYP	DTQETCEAAV	VKLKAGDIV	LVKPGETIP	VDGTVLEGSSAV
a704	AAERLVKLI	PAFCHHMPDYP	DTQETCEAAV	VKLKAGDIV	LVKPGETIP	VDGTVLEGSSAV
	310	320	330	340	350	360
	370	380	390	400	410	420
m704.pep	NESMLTGESLP	PAKMPSEKVTAG	TNTQSPLI	I	RTDRTGGG	TRL
a704	NESMLTGESLP	PAKMPSEKVTAG	TNTQSPLI	I	RTDRTGGG	TRL
	370	380	390	400	410	420
	430	440	450	460	470	480
m704.pep	TAELEQYASSF	IFGELL	LAVPV	FIGW	TLYADAHTAL	WITVALLVIT
a704	TAELEQYASSF	IFGELL	LAVPV	FIGW	TLYADAHTAL	WITVALLVIT
	430	440	450	460	470	480
	490	500	510	520	530	540
m704.pep	AAS	TGTLAREGIL	IGGKQAIET	LAQTTD	IIFDKT	GTLTQGKPAVRRIS
a704	AAS	TGTLAREGIL	IGGKQAIET	LAQTTD	IIFDKT	GTLTQGKPAVRRIS
	490	500	510	520	530	540
	550	560	570	580	590	600
m704.pep	VAQALEQQSEH	PLARAILNCRIS	DG	SV	PDIAIKQRLNR	IGEGVGAQLTVNGETQVWALGR
a704	VAQALEQQSEH	PLARAILNCRIS	DG	SV	PDIAIKQRLNR	IGEGVGAQLTVNGETQVWALGR
	550	560	570	580	590	600
	610	620	630	640	650	660
m704.pep	ASYVAEISGKEP	QTEGGGSAVY	LGSQSGFQAVFY	LTDP	PKDSAAEAVRQ	LAGKNLTLHIL
a704	ASYVAEISGKEP	QTEGGGSAVY	LGSQSGFQAVFY	LTDP	PKDSAAEAVRQ	LAGKNLTLHIL
	610	620	630	640	650	660
	670	680	690	700	710	720
m704.pep	SGDRETAVAET	ARALGVAHYRAQ	AMPEDKLEYV	KALQKEGK	KVLMIGD	GINDAPVLAQAD
a704	SGDRETAVAET	ARALGVAHYRAQ	AMPEDKLEYV	KALQKEGK	KVLMIGD	GINDAPVLAQAD
	670	680	690	700	710	720
	730	740	750	760	770	780
m704.pep	VSAAAAGGT	DIARDGADIV	LLNEDLRTVAH	LLDQARRTRHI	IRONLIWAGAYNII	AVPLA
a704	VSAAAAGGT	DIARDGADIV	LLNEDLRTVAH	LLDQARRTRHI	IRONLIWAGAYNII	AVPLA
	730	740	750	760	770	780
	790	800	810	820		
m704.pep	VLGYVQPWIA	AALGMSFSS	LAVLGNALRLH	KRGKM	QSEKMPSEQX	
a704	VLGYVQPWIA	AALGMSFSS	LAVLGNALRLH	KRGKM	QSEKMPSEQX	
	790	800	810	820		



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

```

g705.seq
1  GTGTTCAATA ATTTCCttgc CTCTCTGCCG TTTATGACGG AAACACGCGC
51  TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTAAAGCC GGCTTTACAG
101 TGTCTTtgcC TTTGGCGATC GCTTCTTTCG TTATCGGCAT GATTATTGCC
151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTTCCAAAA
201 ATGCTTGTtG AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
251 CGCTGTtGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC GTCCGTCGGC
301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCGATTTTG TCCGTGCCGA
401 AAGGGCAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCACC GCAGGCATTC CGCGTCGCCG TTCCGCCGTT
501 GAGCAACGAG TTTATCGGCT TGTTCAAAAA CACCTCGCTT GCCGCCGTGG
551 TAACGGTAAC GGAGCTTTTC CGTGTGCGAC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGGTTT ATTGGTGTtT
651 CTGTAAAGTG CTGTTTTTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GTTATGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

```

g705.pep
1  VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51  VAVALVRIMP SGGIFQKCLL KLVEFYISVV RGTPLLVLQV IVFYGLPSVG
101 IYINPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIQARLEK RFDRYVAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```

m705.seq
1  GTGTTCAATA ATTTCTTGcC TTCGCTGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTTG CTTTGGTGGC GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTtGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TTGTCGCGCC GCAGGCATTC CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGCTCA TATCGAAGCC GCTTTGTTTT ACTGGTGTtT
651 TTGTAAAGTG CTGTTCTCTG TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```

m705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLQV IVFYGLPSVG
101 IYIDPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLIQARLEK RFDRYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```

m705/g705    95.0% identity in 238 aa overlap

          10      20      30      40      50      60
m705.pep    VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
          |||||:::|||||:|||||:|||||:|||||:|||||:|||||
g705         VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP
          10      20      30      40      50      60

          70      80      90      100     110     120
m705.pep    AGGIVRKILLKLVEFYISVIRGTPLLVLQVIVFYGLPSVGIYIDPIPAAIIGFSNLVGAY
          :||| :| |||||:|||||:|||||:|||||:|||||:|||||:|||||

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```

g705      SGGIFQKCLLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
m705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           |||
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA  ATTCCTTGC  TTCGCTGCCG  TTTATGACGG  AAACACGCGC
51 CGATATGATT  GTCAGCGCGT  TTTTGCCTAT  GGTCAAAGCC  GGCTTCGCGG
101 TCTCTCTGCC  TTTGGCGGCA  GCTTCTTTCG  TTATCGGTAT  GATGATTGCG
151 GTAGCCGTGG  CTTTGGTGGC  GATTATGCCC  GCCGGCGGCA  TCGTGCGGAA
201 AATCCTGCTG  AAATTGGTGG  AATTTATAT  TTCCGTCATT  CGCGGTACGC
251 CGCTGTTGGT  TCAGCTTGTG  ATTGTGTTT  ACGGGCTGCC  TTCCGTCGGC
301 ATCTATATCG  ACCCGATTCC  TGCCGCCATC  ATCGGCTTTT  CGCTCAATGT
351 CGGCGCATAT  GCTTCCGAAA  CCATACGCGC  GGCAATTTTG  TCCGTACCGA
401 AAGGCCAATG  GGAAGCAGGT  TTCTCCATCG  GCATGACCTA  TATGCAGACG
451 TTCCGCCGCA  TCGTCGCGCC  GCAGGCATT  CGCGTTGCCG  TGCCGCCTTT
501 GAGCAACGAG  TTTATCGGTT  TGTTAAAAA  CACCTCGCTC  GCGGCAGTCG
551 TGACGGTAAC  GGAATTATTC  CGCGTCGCGC  AGGAAACGGC  AAACCGCACT
601 TATGACTTTT  TGCCCGTCTA  TATCGAAGCC  GCTTTGGTTT  ACTGGTGTTC
651 TTGTAAAGTG  CTGTTCTCTG  TTCAGGCGCG  TTTGGAAAAA  CGTTTCGACC
701 GCTACGTCGC  CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP  FMTETRADMI  VSAFLPMVKA  GFAVSLPLAA  ASFVIGMMIA
51 VAVALVRIMP  AGGIVRKILL  KLVEFYISVI  RGTPLLVLQV  IVFYGLPSVG
101 IYIDPIPAAI  IGFSNLVGAY  ASETIRAAIL  SVPKGQWEAG  FSIGMTYMQT
151 FRRIVAPQAF  RAVVPPLSNE  FIGLFKNTSL  AAVVTVTELF  RVAQETANRT
201 YDFLPVYIEA  ALVYWCFCVK  LFLIARLEK  RFDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

           10      20      30      40      50      60
a705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           |||
m705      VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           10      20      30      40      50      60

           70      80      90      100     110     120
a705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIAAIIGFSLNVGAY
           |||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
a705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
m705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
a705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           |||
m705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq  
 1 ATGAACCTCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA  
 51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCGgaa  
 101 ccgtCCTGTT CGCCACCGCA CTCGCCCGgc tACTCCACCT CCAacacggc  
 151 gAATGGATAG GGAtgaCCGT CTTCTGTCGTC CTCGGCATGC TCCAGTTCCA  
 201 AGGCGcgatt tActccaacg cgggtGAacg taTGctcggg acgggtcatcg  
 251 ggctgGGCGC GGGTTTGGgc gTTTTATGGC TGAACCAGCA TTAttccac  
 301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg  
 351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA  
 401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC  
 451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC  
 501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG  
 551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC  
 601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA  
 651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG  
 701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC  
 751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT  
 801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT  
 851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCGCCCT CATCAACGGC  
 901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA  
 951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA  
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC  
 1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG  
 1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep  
 1 MNSSQRKRLS GRWLSYERY RHRRLIHAVR LGGTVLFATA LARLLHLQHG  
 51 EWIGMTVFVV LGMLQFQGA I YSNAVERMLG TVIGLGAGLG VLWLNQHYFH  
 101 GNLLFYLTIG TASALAGWAA VGKNGYVPM L AGLTMCMLIG DNGSEWLDSG  
 151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLAD SKMIAEISNG  
 201 RRMTRERLEQ NMVKMRQINA RMVKSRS L AATSGESRISP SMMEAMQHAH  
 251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTALING  
 301 RHARRIRIDT AINPELEAL EHLHYQWQGF LWLSTNMRQE ISALVILLQR  
 351 TRRKWLDAHE ROHLRQSLLE TREHG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq  
 1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA  
 51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG  
 101 CCGTCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC  
 151 GAGTGGATAG GGATGACCGT CTTCTGTCGTC CTCGGCATGC TCCAGTTTCA  
 201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTTCATCG  
 251 GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC  
 301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG  
 351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA  
 401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA  
 451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC  
 501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG  
 551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC  
 601 AGGCGCATGA CCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA  
 651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCATCTCGCC GCCACATCGG  
 701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC  
 751 CGTAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT  
 801 GCAATCTCCC AACTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT  
 851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC  
 901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA  
 951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA  
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC  
 1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG  
 1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep  
 1 MNTSQNRNLV SRWLSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG  
 51 EWIGMTVFVV LGMLQFQGA I YSKAVERMLG TVIGLGAGLG VLWLNQHYFH  
 101 GNLLFYLTIG TASALAGWAA VGKNGYVPM L AGLTMCMLIG DNGSEWLDSG  
 151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLAD SKMIAEISNG  
 201 RRMTRERLEE NMAKMRQINA RMVKSRS L AATSGESRISP AMMEAMQHAH  
 251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING

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301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR  
 351 TRRKWLDAHE RQHLRQSLLE TREHG\*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQRNRLVSRWLSYERYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	MNSSQRKRLSGRWLSYERYRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAIYSKAVERMLGTVIGLGAGLVWLNLQHYFHGNLLFYLTVGTSALAGWAA					
g706	LGMLQFQGAIYSNAVERMLGTVIGLGAGLVWLNLQHYFHGNLLFYLTIGTSALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAKLLPLKSTLMWR					
g706	VGKNGYVPMLAGLTMCLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMAIEISNGRRMTREERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
g706	FMLADNLADCSKMAIEISNGRRMTREERLEENMVKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTELLTTAAKLQSPKNGSEIRLLDRHFTLLQTDLQQTVALING					
g706	SMMEAMQHAHRKIVNTELLTTAAKLQSPKNGSEIRLLDRHFTLLQTDLQQTAAALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
g706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRKWLDAHE					
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHGX					
g706	RQHLRQSLLETREHGX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTGGGC	GTTTATGGC	TGAACCAGCA	TTATTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACGGC

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901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG
1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
  1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFQGA IYSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG
151 LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

	10	20	30	40	50	60
a706.pep	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a706.pep	LGMLQFQGA IYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVGTASALAGWAA					
m706	LGMLQFQGA IYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVGTASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a706.pep	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a706.pep	FMLADNLDC SKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
m706	FMLADNLDC SKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
	250	260	270	280	290	300
	310	320	330	340	350	360
a706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
	310	320	330	340	350	360
	370					
a706.pep	RQHLRQSLLE TREHSX					
m706	RQHLRQSLLE TREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

## m707.seq

```

1   ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TGCGGGCGGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTTGT TTTATGTTTC ATATGGACGC
751 GGTTTGGCGC ACAAACCGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCAATTA TTCGGTGCCG GTAAAAAAT
851 GGCTGTTTTT TTTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCATTCCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCCGCCGAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCCG CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAC
1151 GCGGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGA
1251 CGCAGCCGCC CCATTTATTT TAGGCAAAAC GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGCGA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCCG
1551 CTTCAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

## m707.pep

```

1   MEIINDAELI RSMQRQOHID AELLTDANVR FEQPLEKNNY VLSEDETPTCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSQA IIQPNMDSG ILKLRVSAGE IGDRIYEEKR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRLRP SVKTDIQUIP SEEEGKSDLQ
201 IKWQONKPIR FSIQIDDAGG KTTGKYQGNV ALSFDNPLGL SDLFYVSYGR
251 GLAHRDLDLD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAEHLRHRAY LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRMK IITASLDAAA PFILGKQOFF YATAIQAWN KPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

## a707.seq

```

1   NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTC GGGAAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAGAAC TGCGTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NNTAAGCGAT TNGTTTTATG TTTCATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAG CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNCCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```

1139

```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
  1 XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
 51 KLRVSAGEIG DIRYEEKRDY KSAEGSISAF NNKXPLYRNL ILNLRDVEQG
101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAERML
251 LWXXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRRSAGWE AELRHAYLX
301 RWQLDGKLSY KRGTGMRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGRFGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                         XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
                                         |||
m707      EDETPCTRVNYSISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
              50      60      70      80      90      100

a707.pep              40      50      60      70      80      90
GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDYKSAEGSISAFNNKXPLYRNLKI
|||
m707      GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKXPLYRNLKI
              110     120     130     140     150     160

a707.pep              100     110     120     130     140     150
LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
|||
m707      LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
              170     180     190     200     210     220

a707.pep              160     170     180     190     200     210
GKYQGNVALSXDNPGLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
|||
m707      GKYPGNVALSFDNPGLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRYSVHYSVPVKK
              230     240     250     260     270     280

a707.pep              220     230     240     250     260     270
WLFSEFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
|||
m707      WLFSEFNHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKTSGVMKWLWTRQTY
              290     300     310     320     330     340

a707.pep              280     290     300     310     320     330
KYIDDAEIEVQRRRSAGWEAELRHAYLXRWQLDGKLSYKRGTGMRQSMPEPEENGGGTI
|||
m707      KYIDDAEIEVQRRRSAGWEAELRHAYLNRWQLDGKLSYKRGTGMRQSMPEPEENGGDIL
              350     360     370     380     390     400

```

	340	350	360	370	380	390
a707.pep	PXXSRMKIITAGLDAAAPXMLGKQOFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
m707	PGTSRMKIITASLDAAAPFILGKQOFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG					
	410	420	430	440	450	460
a707.pep	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
m707	EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK					
	470	480	490	500	510	520
a707.pep	VGGMFAYDLFAGKPLHKPKGFQTNTNYGFNLNYSFX					
m707	VGGMFAYDLFAGKPLHKPKGFQTNTNYGFNLNYSFX					
	530	540	550	560		

```
g708.seq
1 ATGCCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCCT
51 GGGCGCGTGC AGCACTTCCT ACCGCCCTCT CGCGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCCCTGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGAAGCCCTT CTCCATCAA
301 CCCGACAGTG CCGAAATCAA CAACAACATA GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA AGCCTATGCG
401 ACCCCACCTA CCGACCCCTT TATATTGCCA ACCTGAATAA GGCTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCGCGC CAGCCGCGAG TCCCACCCGC ATTTAAAGAA CTGGCGGCCA
551 CCAAAATGCT GGCCGGGCGA TTGGCGGATG CCGATTACTA CTTTAAAAAT
601 TACCAAAAGC GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTT
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCTC
751 ACCGGTCAAT AA
```

**g708.pap**

1	MPFKPSKRIS	LLVLVLAGAC	STSYRPSRAE	KANQVSNIKT	QLAMEYMRGQ
51	DYRQATASIE	DALKSNPKNE	LAWLVRAEII	QYLKVNDKAQ	ESFRQALSII
101	PDSAEINNNY	GWFLCGRLLR	PAESMAYFDK	ALADPTYPTP	YIANLNKGIC
151	SAKQGQFGLA	EAYLKRLSAA	QPQFPFAFKE	LARTKMLAGQ	LGDA DYFFKK
201	YQSRVEVLQA	DDLLL GWKIA	KALGNVQAAY	EYEAQLQANF	PYSEELQTVL
251	TQSR*				

```
m708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCCT
51  GGGCGCGTGC AGCACTTCTT ACCGCCCTCT CGCGGCAGAA AAAGCCAATC
101 GGGTTTCCAA TATCAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGCCGCAG GAAAGTTTCC GGAAGCCCTT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACAC GGTGTGTTCC TATCGGCGAG
351 GCTCAACCGC CTTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCGACCCCTT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAATGCTT GCGCCGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAGACA GGGTAGAAGT CTTACGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GCGCGCATAC GAATATGAAG
701 CACAATTGCA GCGCAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTGAAT AA
```

m708.per



1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVR AEIY QYLKVNDKAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGR LNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRS LAA QPQFPFPAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLLV LALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              |||
g708           MPFKPSKRISLLLV LALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90      100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLKVNDKAQESFRQALSIKPD SAEINNNYGWFLCGR LNR
              |||
g708           DALKSNPKNELAWLVRAEIYQYLKVNDKAQESFRQALSIKPD SAEINNNYGWFLCGR LNR
              70      80      90      100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRS LAAQPQFPFPAFKE
              |||
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRS LAAQPQFPFPAFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLL LGWKIAKALGNAQAAYEYEAQLQANF
              |||
g708           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLL LGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
              |||
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGCGAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAAC TAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2378; ORF 708.a&gt;:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVR AEIY QYLKVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGR LNR PAESMAYFDK ALADPTYXP YIANLNKGIC
151 SAKQGQFGLA EAYLKRS LAA QPQFPFPAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDL LLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQXLSIKPDSAEINNNYXWFLCGRLNR					
m708	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQALSIPKPSAEINNNYXWFLCGRLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51  CGTCGCTCGT GCTCTGATTG CCGCAATGGG CTATACCATC ATTTCAATTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CCGCGCGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGCGT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCCGACT TATTTTATT TTTCGCCCTT
351 CCGCTGTGTT TCCGTCATCG GCGTGTCCAT CCGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGgcggg cgcgattgTT tccggTGTGT TTTTCGGCGA
501 TAAATGTCC CCGCTTTCCG ACACCACGGG CATTTCGCGC TCCATCGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 GCGTGGCTTA TCAGCGCGGC ACTGATGCTT TGGCTTCTTC CCAGCGTCGC
651 CCGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTTGG GCACGGCTAT TCGCTGATTC CGTTTGCAT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCCATGCTCT TTACCGTCAT
801 TTCCGCGCGT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTATGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GACATTGCCA AACTGATTTT CCGCGGCGGC TTGGAGAGTA TGTCTTTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGGCG
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCGG TCCGTACCTT CTGACGAAT
1051 GCCGGACGCG CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTCAATTT
1101 CCTGATTGGA GAGCAATATT TGAGCATCCT GCTTTCGGGA GAAACGTTCA
1151 AACCCGTTTA CGACAACTC GGCCTGCATT CGTGCAACCT GTCGCGGACT
1201 CTGGAAGATG CGGGACGGT GATTAACCCG CTCGTGCCGT GGAGCGTGTG
1251 CGGCGTATTT ATCAGCCACG CCCTTGGCGT ACCCGTTTGG GAATATCTGC
1301 CTTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTAACCTT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQAGMIGAL NQGMGAVYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGILSPT YFYFSAFALC SVIGVSISS LTACATVGVA FMGMAAFOA
151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFH IKNNMYTTIP
201 AWLISAALML WLLPSVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVV
251 LALMRVNAV AVMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAVRTFLTN

```

1143

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT  
 401 LEDAGTVINP LVPWSVCGVF ISHALGVVPW EYLPYAFFCY LSLALTLFLG  
 451 WTGLTLSKK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq  
 1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC  
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTGG  
 101 AGTGGTTGCG GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG  
 151 TACGGCTTGG CCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT  
 201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACTTGTTC TTCTTCATCG  
 251 GCGTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG  
 301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTATT TTTCTCCTT  
 351 CCGCTGTGT TCCGTTCATG CCGTGTCCAT CCGCAGCAGC CTGACCACCT  
 401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC  
 451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGGCGCAT TTTTGGCGA  
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG  
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC  
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTCCG  
 651 CCGCGAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA  
 701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTGCGCT GTTGGTCATT  
 751 TTGGCATTGA TGCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT  
 801 GGTGTCCGTT GCTGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC  
 851 TCGGTGCGTG GTTTACGGC GGCTACAAAC TCGAAGCGA AGCGTTTAAA  
 901 GATGTTGTCA AACTGATTTC GCGCGGCGGT TTGGAAAGTA TGTTTTTCAC  
 951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTGCGC  
 1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT  
 1051 GCCGGACGCG CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTTAATTT  
 1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCGGGT GAAACGTTCA  
 1151 AACCCTGTTA CGATAAGCTC GGTCTGCATT CCGCAATCT CTCGCGGACG  
 1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG  
 1251 CGGCGTGTTT ATCAGCCACG CGCTGGCGCT GCCGGTTTGG GAATATCTCG  
 1301 CGTATGCCTT TTTCTGCTAT TTGAGTTGG CTTTGACCCT GTTATTCGGT  
 1351 TGGACGGGGC TGACTTTGAG CAAAAAATA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep  
 1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL  
 51 YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM  
 101 YYGFGLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQA  
 151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFHE IKNMYYTIP  
 201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI  
 251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK  
 301 DVVKLISRGG LESMFFTQTI VILGMSLGL LFALGVIPSL LEAIRFTLN  
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST  
 401 LEDAGTVINP LVPWSVCGVF ISHALGVVPW EYLPYAFFCY LSLALTLFLG  
 451 WTGLTLSKK\*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQGMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSSFALC					
g709	DMQAGMIGALNQGMGAVYLF FFIGLMVSALMMSGAIPTLMYYGFGLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVA FMGMAAFQADAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVA FMGMAAFQADAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFHEIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFHEIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
m709.pep	SIVGIDLFHEIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFHEIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLF	TVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
g709	SLIPFALLVVLALMRVNAVVM	LFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMFFTQ	TIVILGMSLGGLLFALGVIPSLLEAIRTFTLNAGRATFSVAM				
g709	DIAKLISRGGLESMFFTQ	TIVILGMSLGGLLFALGVIPSLLEAVRTFTLNAGRATFSVAM				
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNL	SRTLEDAGTVINPLVPSVCGVF				
g709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSCNLS	SRTLEDAGTVINPLVPSVCGVF				
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWGTGLT	LSKKX				
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWGTGLT	LSKKX				
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CGGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGNCGCAT TNTTNGGCGN
501 CAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACACG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGCCTT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTC TCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTGAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCTNGG GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTC ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGLISPT YFYFSAFALC SVIGVSIGSS LTTTCATVGVA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXSA SIVGIDLFH IKNMMYTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV VAMLFVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMFFTQTI VILGMSLGG L FALGAIPSL LDAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNL SRT

```

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG  
 451 WTGLTSLKK\*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTII	XLEWLP	PHMSII	AAIVVL	LILYGL	LARGLKYN
m709	MFAFXSLDMPRGEALAVVVALIAAMGYTII	SLEWLP	PHMSII	AAIVVL	LILYGL	LARGLKYN
	10	20	30	40	50	60
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMGAIY	LEFFIG	LMVSAL	MMSGAI	PTLMYY	GFGGLISPTYFYFSAFALC
m709	DMQQGMIGALNQGMGAIY	LEFFIG	LMVSAL	MMSGAI	PTLMYY	GFGGLISPTYFYFSSFALC
	70	80	90	100	110	120
	130	140	150	160	170	180
a709.pep	SVIGVSIGSSLTTCATVGV	AXMGXXX	AFXAXMXXXXX	IVXXAXX	GXKMSPL	SDTXGXA
m709	SVIGVSIGSSLTTCATVGV	AFMGMAAFQ	ADMAMTAGA	IVSGAFF	GDKMSPL	SDTTGISA
	130	140	150	160	170	180
	190	200	210	220	230	240
a709.pep	SIVGIDLFEHIKNMMYTTI	PAWLIS	XXLMLX	LLPSVAA	QDLNSVES	FRSQLEATGLVHCY
m709	SIVGIDLFEHIKNMMYTTI	PAWLISA	ALMLWL	LPNVAA	QDLNSVES	FRSQLEATGLVHG
	190	200	210	220	230	240
	250	260	270	280	290	300
a709.pep	SLIPFALLVVLALMRVNA	VAMLF	TVIAA	VA	TYLHST	PDRLQLGAWFYGGYKLEGEAXX
m709	SLIPFALLVILALMRINAV	VAMLF	TVMVAV	AVTYLH	STPDRLQ	LGAWFYGGYKLEGEAFK
	250	260	270	280	290	300
	310	320	330	340	350	360
a709.pep	DIAKLISRGGLISMFFTQ	TIVILG	MSLGG	LLFALG	AIPSL	LDVRSFLT
m709	DVVKLISRGGLISMFFTQ	TIVILG	MSLGG	LLFALG	VIPSL	LEAIR
	310	320	330	340	350	360
	370	380	390	400	410	420
a709.pep	TSVGVNFLIGEQYLSILL	SGETFK	PVYDKL	GLHSRNL	SRTLE	DAGTVINPLVPWSVCGVF
m709	TSVGVNFLIGEQYLSILL	SGETFK	PVYDKL	GLHSRNL	SRTLE	DAGTVINPLVPWSVCGVF
	370	380	390	400	410	420
	430	440	450	460		
a709.pep	IXHALGVPVWEYLPYA	FFCYLS	ALTLL	FGWTGL	TSLKKX	
m709	ISHALGVPVWEYLPYA	FFCYLS	ALTLL	FGWTGL	TSLKKX	
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq  
 1 ATGGAACCC ACGAAAAAT CCGCTGATG CGCGAATTGA ATAAATGGTC  
 51 CCAGGAGGAT ATGCGGAAA AGCTGGCGAT GTCGCGAGGC GGGTATGCCA  
 101 AAATCGAACG GGGCGAAACG CAGTTAAATA TCCCGCGTTT GGAGCAGTTG  
 151 GCTCAGATT TCAAAATCGA TATGTGGGAC TTGCTCAAAT CGGGCGGTGG  
 201 TGGGATGGTG TTTCAGATTA ATGAAGGTGA TAGTGGTGGC GATATTGCGT  
 251 TGTATGCGTC GGGTGTGTT TCGATGAAAA TAGAATTTTT AAAAATGGAG

m710.pep

a710.seq

a710.pep

	10	20	30	40	50	60
a710.pep	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD					
m710	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a710.pep	LLKSGGGGMVLQINDVDTSNGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKEIELLR					
m710	LLKSGGGGMVFAQINEGDSG-GDIALYASGDVSMKIEFLKMELKHCKEMLEQKDKEIELLR					
	70	80	90	100	110	

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```

1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTGCGCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACGCTA
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTGGC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAE YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDDYNAGRM
251 NYRPDLKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTGCGCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTACCC GCCCAACGGC TACAACGCTA
551 GTTGTCTGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
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1148

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901   CCGGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951   TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001  TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051  GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101  GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151  TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201  ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251  CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

**a711.pep**

```

1   MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSlyTTD RGFdYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

**a711/m711 99.8% identity in 431 aa overlap**

	10	20	30	40	50	60
a711.pep	MPAPDLGFALS LPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALS LPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a711.pep	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a711.pep	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a711.pep	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSlyTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSlyTTD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a711.pep	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEVKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEVKQRLDIDGK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a711.pep	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
	370	380	390	400	410	420
a711.pep	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420



a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```

m712.seq
1   ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATTG GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACC GTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACC GCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GCGGTGCGCA AAAATGCGGA CATTGCCACG GCCTTGTTCA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACGAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GCGGTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401 TTTGATTTTG TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2394; ORF 712&gt;:

```

m712.pep
1   MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKQVL MVAPMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHL MVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSNNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLIKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADV VNG LH VFAGRIDLIL *

```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACC GC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTTGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCGCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CCGAGGTAC
651 TTTTTTGGCG CAATCGCACG GCCGACGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2396; ORF 713&gt;:

```

m713.pep
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 ERQALTHIAN SVGLHPWLEP DGLTVVGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLLA QSHGRSGDSA KHDWKWYKD PTMTLHREPKT
251 VVVSADADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGGK GKKQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACC GC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTTGGGGCC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCGCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CTGAGGTAC
651 TTTTTTGGCG CAATCGCACG GCCGACGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGATGGA TGGCACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```

1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

**a713.pep**

```

1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFD FVIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVVGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTF LAQSHGRSGDSA KHD LKWVYKD PTMTLHRPKT
251 VVVSADADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGV LWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMLS RMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAETAVF E*

```

**a713/m713 98.4% identity in 381 aa overlap**

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFD FVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFD FVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGRELSSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIAN SVGLHPWLEPDGTLLVVGVD					
m713	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIAN SVGLHPWLEPDGTLLVVGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVTF LAQSHGRSGDSAKHDLKWVYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTF LAQSHGRSGDSAKHDLKWVYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHRPKTVVVSADADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGV LWQPGQR					
m713	PTMTLHRPKTVVVSADADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGV LWQPGLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGI DAVFFLMGRRFMLS RMDGTQ TELRLKEDGI WTPDAYPKKAE AARKRKGR					
m713	VHVIDDEHGI DAVFFLMGRRFMLS RMDGTQ TELRLKEDGI WTPDAYPKKAE AARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVSHKGKKGKKQAETAVFEX					
m713	KGVSHKGKKGKKQAETAVFEX					
	370	380				

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```

m714.seq
  1 ATGAGCTATC AAGACATCTT GCGGGGCTG TTGCCCCCG TGTCGTATGC
 51 CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
201 CCGTACGGGC AAAAACC GCCGACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATCCGCGGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CTACCGCTA A

```

This corresponds to the amino acid sequence &lt;SEQ ID 2400; ORF 714&gt;:

```

m714.pep
  1 MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
 51 RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```

a714.seq
  1 ATGAGCTATC AAGACATCTT GCGGGGCTG TTGCCCCCG TGTCGTATGC
 51 CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
201 CCGTACGGGC AAAAACC GCCGACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATCCGCGGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A

```

This corresponds to the amino acid sequence &lt;SEQ ID 2402; ORF 714.a&gt;:

```

a714.pep
  1 MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
 51 SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPRSAGQMLADW					
	10	20	30	40	50	60
	70 80 90 100 110 120					
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	70	80	90	100	110	120
	130 140 150 160 170 180					
a714.pep	AGDRLAPQEI MWVWHVNVVRG GNNRITRFRAGISAAGDRLTDYSDAVIESL FNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWVHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA  
130 140 150 160 170 180

a714.pep IRFTYRX  
|||||||  
m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq  
1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA  
51 GCGGCTTGCG AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT  
101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT  
151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC  
201 GGGTCGCTCG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC  
251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG  
301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT  
351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT  
401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep  
1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR  
51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGNTIV YAAIHNFGGM  
101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq  
1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA  
51 GCGGCTTGCG AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT  
101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT  
151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC  
201 GGGTCGCTCG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC  
251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG  
301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT  
351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT  
451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep  
1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR  
51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGNTIV YAAIHNFGGM  
101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP\*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq  
1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT  
51 GGCCGCCGGC GCCGTGCGC CCCACAAACC GGCAAGCAAC GCAACAGGCG  
101 TTCAAAAAAT CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT  
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC  
201 TAAAGCAGGC GAAGGCAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA  
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC  
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep  
1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG  
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

101 EGKCGEGKCG SK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq  
 1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT  
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG  
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT  
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG  
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA  
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT  
 301 TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep  
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHNSAHG SCGASKSAEG  
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG  
 101 SK\*

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGA-----				
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQGSAGASKSAEGSCGASKSAEG				
	10	20	30	40	50
	60	70	80	90	100
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
	(:				
g716	SCGAASKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq  
 1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT  
 51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG  
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT  
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG  
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA  
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT  
 301 TCTAAATAA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep  
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHNSAHG SCGASKSAEG  
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG  
 101 SK\*

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHNSAHGSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq  
 1 ATGGACACAA AAGAAATCCT CGGTACGCG GCAGGCTCGA TCGGCAGCGC

```

51  GGGTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTCTG  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCTGTA  CGCCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CCGCGCCCGT  TTTCCGCCGC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCCGTGC  AATCGAAGAA  AACGCCACGC
851  CGCGCCGCCCT  CTCGGCAACG  GCAGAAATCCG  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGccgc
1001  cgtGTTTGA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CTTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTGCTGCTG  TGCCGCCTCA  TTCTGGTGTG  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTTC  TGCTGTCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCcctgttt  gccggcgtAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCTGCG  GCCACCGGAA  AAATTTGCAC  AAATGTTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

```

g717.pep
1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCLGLDQA  YVREYYAAAD  KDTLFKTLFL  PPLIFSAAIA  ALLLSRPSLP
101  SEILFSLDDA  AAGIGLVLFE  LSELPPIRFL  LVLRMEGRAL  AFSSAQLVPK
151  LAILLLLPLT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCLKAVR
201  RPFSPAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKXY  AGLEQLGVYS
251  MGISFGGAAL  LLOSIFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGFESP  LASLLLPENY  AAVRFTVWSC  MLPLFYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALAAANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFFVFKTE
401  SSCRLWQPLK  RLPLYMHTLF  CLASSAAYTC  FGTPANYPLF  AGVWAAAYLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

```

m717.seq
1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGGTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCGGCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAAC  CCTGTTCTCTG  CCGCCGCTGC
251  TGTTGCTCCG  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCTGTA  CGCCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CACGCACCGT  TTTCCGCCGC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CGCGCCGCCCT  CTCGGCAACG  GCAGAAATCCG  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCCTCC  TCCTGCTGCC
951  GGAAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTGA  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCGATCGC  GCTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CTTGCTGCTG  CTGGGGCTTG  CCGTGCCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTGCTGCTG  TGCCGCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTTC  TGCTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTTT  GCCGGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCTGCG  GCCACCGGAA  AGATTTGCAC  AAATGTTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```



This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

```

m717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFKTLFL PPLLSAAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLEF LSFLPIRFLF LVLRMEGRAL AFSSAQLVPE
151 LAIIIIIIPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRFIALAT LGALAANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

m717/g717 96.4% identity in 473 aa overlap

      10      20      30      40      50      60
m717.pep MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
g717      MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
      10      20      30      40      50      60

      70      80      90     100     110     120
m717.pep YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF
g717      YVREYYAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF
      70      80      90     100     110     120

      130     140     150     160     170     180
m717.pep LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAIIIIIIPLTVGLLHFPANTAVLTAVYALA
g717      LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAIIIIIIPLTVGLLHFPANTSVLTAVYALA
      130     140     150     160     170     180

      190     200     210     220     230     240
m717.pep NLAAAFLLFQNRCLKAVRHAPFSPAVLHRGLRYGIPIALSSIAIWGLASADRLFLKKY
g717      NLAAAFLLFQNRCLKAVRRAPFSPAVLHRGLRYGIPIALSSIAIWGLASADRLFLKKY
      190     200     210     220     230     240

      250     260     270     280     290     300
m717.pep AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
g717      AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS
      250     260     270     280     290     300

      310     320     330     340     350     360
m717.pep ALCLTGIFSPLASLLPENYA AAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT
g717      ALCLTGIFSPLASLLPENYA AAVRFIVVSCMLPPLFCTLA EISGIGLNVVRKTRPIALAT
      310     320     330     340     350     360

      370     380     390     400     410     420
m717.pep LGALAANLLLGLAVPSGGARGA AAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
g717      LGALAANLLLGLAVPSGGTRGA AAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
      370     380     390     400     410     420

      430     440     450     460     470
m717.pep CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX
g717      CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHLYLKKQGFPLX
      430     440     450     460     470

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

```

a717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTCT CCGCCGCTGC

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1158

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTGCGT CGACGATGCC GCCGCCGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
401 GTATGGAAGG ACGCGCCTT GCCTTTTCGT CCGCGCACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GCGGAACACC GCCGTCTGA CCGCGTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGTCTGAA GGCCGTCCG
601 CGCGCACCGT TTTTCATCCG CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTTC
751 ATGGGTATTT CGTTCGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCCGC
851 CCGCCCGCCT CTCGGCAACG GCAGATCCG CCGCCGCCCT GCTTGCCCTC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTC GGTTTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTG CACGTGGTA GAAATCAGCG GCATCGGTTT GAACGTGCTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGCTTG CCGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGGTTGCTG TGCCGCTCA TTTTGGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCGC TTTATATGCA
1251 CACATGTTC TGCCTGGCCT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGCAAACTA CCCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGAA AGATTTGCAC AAAGTGTTC ATTATTTGAA
1401 AAAACAAGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLRMERAL AFSSAQLVSK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSIFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGA RGAAVACAAS FWLFFVFKTE
401 SSCRLWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

	10	20	30	40	50	60
a717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
m717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a717.pep	YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
m717	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA					
m717	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a717.pep	NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
m717	NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a717.pep	AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS					

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|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep   ALCLTGIFSPLASLLLPENYA AVR FIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
           |||||
m717      ALCLTGIFSPLASLLLPENYA AVR FIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep   LGALAANLLLLGLAVPSGGARGA AVAC AASF WLF FVFKTESSCRLWQPLKRLPLYMHTLF
           |||||
m717      LGALAANLLLLGLAVPSGGARGA AVAC AASF WLF FAFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep   CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
           ||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAA YLAGCILRHRKDLHKL FHYLKKQGFPLX
           430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1  TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51 GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTC ACCCCAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCTT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTGCAA ATCAACTATC CCCATGCCGA
651 CCAAACCGCG GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCGGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1  SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGVVHTQK
51 SRSVQQARNG LFRTLWLYM FKHYAVHDFE EFLELYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLQMAW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGVO
251 IPESWVRDKL VIPDVQEGEA VLVQRQPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

## a718.seq

```
1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGTACCCG CGAAAATCCG GAAGCGGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTCATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTGCT TCGAGCGGCT GGCGGAAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGACAC AACCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A
```

This corresponds to the amino acid sequence &lt;SEQ ID 2422; ORF 718.a&gt;:

## a718.pep

```
1 MEPIMAKKN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEKLSD QAYEMMDSL P TLEDLIMDL M DAVGHGFSAL EVIEWFSDGL
151 YLPRNFIHRP QSWFKWDKDN G LLLRTREN P EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMA DWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRPVKF EFDTREPKDI AVFADAI PKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDENSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*
```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS	SDGLYLPRNFIHRPQSWFKWDKDNGLLLRT				
m718				SDGLYVPRNFIHRPQSWFKWDKDNGLLLRT		
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLLQMA DW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTATSNPFLLQMA DW					

1161

	100	110	120	130	140	150
	300	310	320	330	340	350
a718.pep	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRDLLVSDAKVAQTITSQIIGPFLQ					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRDLLVSDAKVAQTITSQIIGPFLQ					
	160	170	180	190	200	210
	360	370	380	390	400	410
a718.pep	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVDVGVQIPESWVRDKLVIPDVQEGEA					
m718	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVDVGVQIPESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
	420	430	440	450	460	470
a718.pep	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
	480	490	500	510	520	
a718.pep	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAA ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAATCCG GAAGGGCAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGAAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGGCGCGC TGATTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTGACA CGCGCGAGCC GAAAGACATC GCGGTCCTTG
1151 CCGACGCTAT CCGGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCGA GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDSIDIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEKLSLD QAYENMMSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNRP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRICK YGAGATKEEK
251 NTLRLVAEAI GHNAAGIMPE GMEIELHNAA NGTATSNPFL QMADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```

351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES  
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE  
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL  
501 DNAKLRTYMQ QALFISDILG QDHARA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC  
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG  
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC  
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT  
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC  
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT  
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA  
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG  
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT  
451 TACCTACCCC GAAACTTTAT CCACCGCCCC CAAAGCTGGT TCAAATGGGA  
501 CAAAGACAAC GGGCTGTGTC TGCCTACCCG CGAAAATCCG GAAGGCGAAG  
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC CGCAGCGTC  
601 CAGCAGGCGC GCAACGGGCT TTTCCGACG CTTTCTGGC TGTATATGTT  
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGTGAG CTGTACGGCA  
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA  
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACAAC CGGCAGGCAT  
801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA  
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG  
901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA  
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT  
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC  
1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACCGCGT  
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG  
1151 CCACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCGAAAGC  
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT  
1251 GTTGGTGGCG GAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG  
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGAG GCATCAGGAA  
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCATTC  
1401 TCAGCTCAAC CCGATGGTGC GTCAGCGCGT TGCCGCACTT AATGCTTGCA  
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTG  
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCTTGT TTATCAGCGA  
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA  
51 LFEDAESGDI RAQHELFDI EERDSDIAAN MGRKRALLT LNWRVAPPRN  
101 ATPEEKLSD QAYEMMDSL TLEDLMDLM DAVGHGFSAL EVEWVFSGL  
151 YLPRNFIHRP QSWFKWDKDN GLLRLTREN EGEALWPLGW VVHTQKRSV  
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIG YGAGATKEEK  
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQADWCEKS  
301 AARLILQTL TSGADGKST NALGNIHNEI RRDLLVSDAK QVAQTITSQI  
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES  
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE  
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL  
501 DNAKLRTYMQ QALFISDILG QDHARA\*

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAA	LQTDVAQITATGRVIAEHPS	NFITPQKMRA	LFEDAESGDI		
m718-1	MEPIMAKKNNKTKIQKPEAA	LQTDVAQITATGRVIAEHPS	NFITPQKMRA	LFEDAESGDI		
	70	80	90	100	110	120
a718.pep	RAQHELFDIEERDSDIAAN	MGRKRALLTLNWRVAPPRN	ATPEEEKLSD	QAYEMMDSL		
m718-1	RAQHELFDIEERDSDIAAN	MGRKRALLTLNWRVAPPRN	ATPEEEKLSD	QAYEMMDSL		
	130	140	150	160	170	180
a718.pep	TLEDLMDLMDAVGHGFSAL	EVEWVFSGLYLPRNFIHRP	QSWFKWDKDN	GLLRLTREN		
m718-1	TLEDLMDLMDAVGHGFSAL	EVEWVFSGLYLPRNFIHRP	QSWFKWDKDN	GLLRLTREN		

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVHTQKSRSVQQARNGLFRTLWLYMFKHYAVHDAEFLELYGMPIRIGK					
m718-1	EGEALWPLGWVHTQKSRSVQQARNGLFRTLWLYMFKHYAVHDAEFLELYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMADWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMADWCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDVGVIQIPESWVRDKLVI PDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDVGVIQIPESWVRDKLVI PDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
m718-1	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCGCG	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGCGGC	GCAGCGGCAA	GGCATCACAA	AATGATTTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTGCGGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TGCGCAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTTGGC	ACTTGAACCT	GTGAGAAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AACCAAGAAT	GAAGCGCAGG	CGGCATATGC
651	TTTTGCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTAGACGGC	ACTTTCGAGG	TGCGGGATAT
801	GGTTGCGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTCCG	CGGTTTGGAC	TACCTGCTCT	CACTCTTACA	ATCTGCGGCG
901	AATAAATCGG	GCAGTCCTGC	CGAAGCGGCG	ACTAATGTGC	AAAATCTTTT
951	GAGTAAAACT	CTGTCGCCTG	ACACGATAGG	TCGTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTGCGAT	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGCA	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGGCG	GCGGAGCAGG	CAAATATGCT	TAAGGGCGCG
1201	CTTTTGGCGC	AACTGCTGCC	TGATTTCAG	GCAAAACAAG	GTTTGCTGGC
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGGCTGGCG

1164

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCGAG CCGCGTGGCA GCAGGTGCCA CAGCGGCAGG CCGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAGG GGTTCGCTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCGAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CCGTATCAAG TGGCCATGTT
2151 CGGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

```

m719.pep
  1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
 51 GIRSEKQIQE EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDGG MSGKDLQLGL
251 EHVLSGLDGS TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSGPSAEAA TNVQNLLSKT LSPDTIGRLK KMANPNPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNGK IAKNNEARML
451 SAAQQEQQE SLAMLRESLT GTLVDNETSF KKLAAYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPPE
601 MINRLKNNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

```

m720.seq
  1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCGG
 51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTGTGTCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGTGC
251 TGGTGCACCC TGTTTGGGGG CCGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTT GAAAACGCCCT
401 TTTGGTTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTG TTTGATTTG ACAAATTGC CTTTCCCGAT
601 CGGGGCGGAT ACAGTGCAGC GCGCTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTGCGCCGC ACAGCGGTTT
751 GACGGGGCTG CCGCTGTTGC CGACCGCGCC GCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCGGTTAA

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1165

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATTG ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTTAC GGCGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

**m720.pep**

```

1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WKGKYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEQEIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAI PDNLLTG RFS DGLQNLRL NRLTAKQVQP VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAE SL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

**a720.seq (partial)**

```

1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTGTATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGCGGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGATATC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TCGGCGGCTC ATCAACCAA AGCCGCGCCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

**a720.pep (partial)**

```

1 GLQNLRLNLT AKQVQPVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAAESGGL TANAVYTEAY QTAE SLRAAA
101 GRNLALVA AV INQKPLIVR QAPIDGTI HQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

**m720 / a720 100.0% identity in 169 aa overlap**

```

                250      260      270      280      290      300
m720.pep      SPRQRF DGAAAVADRAAAIPDNLLTGRFSDGLQNLRLNRLTAKQVQPVAQAVRLLSTSSLL
                |||||||
a720          GLQNLRLNLTAKQVQPVAQAVRLLSTSSLL
                10      20      30

                310      320      330      340      350      360
m720.pep      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
                |||||||
a720          SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
                40      50      60      70      80      90

                370      380      390      400      410      420
m720.pep      QTAESLRAAGRLNALVAAVINQKPLIVRQAPIDGTI HQIAHEFYGDIA RAAELVRLNP
                |||||||
a720          QTAESLRAAGRLNALVAAVINQKPLIVRQAPIDGTI HQIAHEFYGDIA RAAELVRLNP
                100      110      120      130      140      150

                430      440
m720.pep      HHHHPAFIKRGTLVNSYAKX

```

a720                   |||||  
                  HIHHPAFIKRGTLVNSYAKX  
                          160           170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq  
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT  
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG  
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA  
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT  
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG  
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG  
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA  
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG  
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT  
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC  
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG  
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC  
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCGC AGCTGGCGGA  
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT  
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC  
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC  
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA  
851 AAGGCGTATT GAAACAGCCG GCGGCGTTGG CATTTTGTAC CGGCTTTATT  
901 GAAAACGCCC AGCCGGTTCG TGCACCTGGC GGCTCGCAAA CGGGCGGCAA  
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG  
1001 CAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC  
1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence &lt;SEQ ID 2434; ORF 721&gt;:

m721.pep  
1 MSKNAQKILL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAYWLTEE  
51 NGHDEVALLAN SSRNQLVVVDY EHOTLYKEKN GOPAPAAGWM RWLEFTPKGM  
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG  
151 MDEVLAASA QILKPETEON PMKELLQOLF DLPDAGEEEL KAALSALVEA  
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV  
251 AALTAKQEAD KGNELITAAL TSGKLLPAOK EWAKGVLKOP GGLAFLTGFI  
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES  
351 EGK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq  
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT  
51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG  
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA  
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT  
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG  
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG  
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA  
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG  
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT  
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC  
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG  
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC  
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCGC AGCTGGCGGA  
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT  
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC  
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC  
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCA  
851 AAGGCGTATT GAAACAGCCG GCGGCGTTGG CATTTTGTAC CGGCTTTATT  
901 GAAAACGCCC AGCCGGTTCG TGCACCTGGC GGCTCGCAAA CGGGCGGTAA  
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG  
1001 CAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence &lt;SEQ ID 2436; ORF 721.a&gt;:

```

a721.pep
1  MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPWYLTEE
51  NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

	10	20	30	40	50	60
a721.pep	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPWYLTEENGHDVALLAN					
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPWYLTEENGHDVALLAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a721.pep	SSRNQLVVDYEHXTLYKEKNQGPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHXTLYKEKNQGPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a721.pep	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
	130	140	150	160	170	180
	190	200	210	220	230	240
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQPPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQPPGGLAFLTGFI					
	250	260	270	280	290	300
	310	320	330	340	350	
a721.pep	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKLGMSGEEFVKIKESGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAMKLGMSGEEFVKIKESGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
1  GTGTTTGAAG CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51  TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCCTCA TGCAGCGCTT GAGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGCGC GCACGCGCGA AATACCGGCA ATCGCCGACG

```

1168

```

401 AGCCGGGCGC GCGCCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

**m722.pep**

```

1 VFETPTFEQI RERILRDTKS LWPDADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPPTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

**a722.seq**

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC GCGGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CGGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TCGCGGGCTT GCGCGCGCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GCGCCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCCGCCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GCGGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

**a722.pep**

```

1 VFETPTFEQI RERILRDTKS LWPDADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPPTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

**g723.seq not found yet**

1169

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```

m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101 TCTTCGCCCC CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201 GGTTCGGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTTC GCAGTGGCGT
351 CCACCAGCGC GGTGTGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTA CTGACC GCCTTGCGTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTTCGCGCCA GCCGCCGTCA AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTTCAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGCGGC GGTTCGCGC GTTTCGGTT
851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2442; ORF 723&gt;:

```

m723.pep
1  MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARETSRQPPS NSRPFPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*

```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```

m724.map
1  ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAAACTGCTAAAAATATCGGCGAAACC
-----+-----+-----+-----+-----+ 60
a  TACTCAAACCTCATTTAACCCTTTTGTGCGGTGTTGACGATTTTATAGCCGCTTTGG
M S L S K L A K K T A Q T A K N I G E T -
61  CTGCGCGCGGCCTTTCGGGGAAAAATCACGCTGGTGGTGTGCTCCGAGCCGATACAGCGC
-----+-----+-----+-----+ 120
a  GACGCGCGCCGGAAGCCCTTTTGTGCGACCAACAGCAGGCTCGGCTATGTGCGG
L R A A F R G K I T L V V S S E P I Q R -
121  GTGCAGTTGAGCGGCTTGCCGACGAAACCTGCAAGACCTTGAACATTTGCAGGAATAC
-----+-----+-----+-----+ 180
a  CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAATTGTAAACGTCCTTATG
V Q L S G L A D E T L Q D L E H L Q E Y -
181  GGCTTTGCCAGCCATCCGCCCCACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
-----+-----+-----+-----+ 240
a  CCGAAACGGTCGGTAGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCGCTTA
G F A S H P P D G S E A V V I P L G G N -

```

1170

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTTCGTGCCGTCGATGGCGTAGTTTTTGGAAATTC
a    T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTTTAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCCACGTTTTTAGCACTAATTCGTTCCGTTT
a    P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a    I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAAGTGCAGTGTTGACGGCGCAA
421  -----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACGCGCGGTT
a    A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATCG
a    G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGCAAT
541  -----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCGTCAAAATTGTGGCTGCCGCTGCACCACCGCCGTTA
a    G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601  -----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCTGTGGGCGTATGGCTGTCTAGCCGCGTTTGAATGGCCGCCTT
a    I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a    P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI  
SalI SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence &lt;SEQ ID 2444; ORF 724&gt;:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTACCGG GTTAAGTGCA
401 AACAATACGA GGTTAATGCG GCCACGGATG CCAAATTTAA CGTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGACCCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQGK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTGDGDDVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

```

              10      20      30      40      50      60
a724.pep      MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
              |||||
m724           MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
              10      20      30      40      50      60

              70      80      90     100     110     120
a724.pep      GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK
              |||||
m724           GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK
              70      80      90     100     110     120

              130     140     150     160     170     180
a724.pep      IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS
              |||||
m724           IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS
              130     140     150     160     170     180

              190     200     210     220
a724.pep      GDVNQTGGSFNTDGDVVGAGNISLRQHPHTDSIGGKTLPAEPAX
              |||||
m724           GDVNQTGGSFNTDGDVVGAGNISLRQHPHTDSIGGKTLPAEPAX
              190     200     210     220

```

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
1  ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
51  GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCGGC GCGTATGCG GACGTTATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGCGCGCA
201 GCGGCAAGGC GGCATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
251 GCGCTGTTTC CCGCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAATAT GACCGTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTACGAC CCGCAATCCG
551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
1  MVRTVKSUNG EADDLAQIHL TPAVWVTYG GSKVEPASTG GVCGRYQDTA
51  EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLL DGQRLGFADS
101 RGLVPKAVRA IANHVLVQNA AVSIYAVEYA IRFNTCGLEN DRYPERTDNP
151 DDPNHIFTKY QGTLSEPWPD FEGLDGKIYD PQSADEIPVN LTLKDKQ*

```

1172

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
  1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
 51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101  CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151  GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201  ATGGAAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251  CCGCCTTGGC ATTCGCCTC GCGGAAAAGG CGGACGAAC CAAAAACAGC
301  CTCTTGCGCG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351  AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401  TGGCGCAAAT CGCCGCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451  AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCCG GCGCGATTAT
501  CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551  CCGGATTGGA CGCGCTGGA AAGGAAATCG AAGAATGGAC GCTAAACATC
601  GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
  1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
 51  VLTFFRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101  LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVLE
151  KVIEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201  G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
  1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
 51  CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101  CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151  GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201  ATGGGAAATC GGCGAAGCCG CTGCCGCGGC CCGTTTCGCC GAACAAAAAA
251  CCGCCACGGC ATTCGCCTC GCGGCAAAGG CGGACGAAC CAAAAACAGC
301  CTCTTGCGCG GCTATCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351  AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401  TGGCGCAAAT CGCCGCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451  AAAGTTGTCT AAAAATCCGC CCGCCTGGCC GTTGCCGCCG GCGCGATTAT
501  CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551  CAGGATTGGA CGCGCTGGA AAGGAAATCG AAGAATGGAC GCTAAACATC
601  GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
  1  MTIYFKNGFY DDTLGSIEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
 51  VLTFFRPSDY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101  LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDLVLE
151  KVVEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
201  G*
```

a726/m726 95.5% identity in 201 aa overlap

```

              10      20      30      40      50      60
a726.pep      MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTFFRPSSEY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726          MTIYFKNGFYDDTLGGIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTFFRPSDY
              10      20      30      40      50      60
```



m727.seq

```
1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTCG GAAGCAGCAG GCGGTCTATC ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAACT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGTC GAAAAAACAG GCGGAAGTCA GCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTTAA
```

m727.pep

1	MNLVKLLANN	WQPIAIIALV	GTGLAVSHHQ	GYKSAFAKQ	AVIDKMERDK
51	AQALLLSAQN	YARELELARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTER
101	DLCKIPFPD	SRNPNTGFR	LFSQIPPNT	QIPP*	

**a727.seq**

```
1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGAACCGA TTGCCATCAT
51 CGCGCTTTGTC GGCACGGGTT TGGCGGTGAT GCACCATCAA GGCTACAAGT
101 CGGCTTTTTCG GAAGCAGCAG GCGGTCTATT AGAAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCCGC AACTGGAACA
201 GGCGCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTGCGCA
251 TGGCTTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGAAAAAT
301 AAAAAGGAAA TCGAAAATTG CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGCTTGATT GACGGCTTGT GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA
```

a727.pep

1	MNLVKLLANN	WQPIAIIALV	GTGLAVSHHQ	GYKSAFAKQQ	AVIEKMKRDK
51	AQALLLSAQN	YARELEQARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTEN
101	KKEIENVLTO	DRKNAGGGCI	DGFGHHGLQL	YKRALGYGN*	

a727.pep MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN

1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
           10      20      30      40      50      60
           70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAEAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDPSRNPNTGF
           70      80      90      100     110
           120     130     140
a727.pep   IDGFGHHGLQLYKRALGYGNX
m727      RLFSPQIPPNFTQIPPX
           120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

g728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTTCGG ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCCG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGCTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACCG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCAACAT CTTGACGCGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCTTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

g728.pep

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGCMQ AOVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGV TADMQT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

m728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCT TGCCGGAACT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

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1175

```

501 CCGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGA AAAACGG AAATCTTTT
901 ATTGCACAAT CTTCGACGGT AGCATTGAAA GCGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GCGGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

**m728.pep**

```

1 MFKKFKPVLL SFFALVF AFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51 AKLARLFRNA DRVVIVKES IRTEENLAGT VDDGPLQSEK DYLA LAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVA VLSQRS PEA FVNAEYL
151 YRND RPF SVN VYGGTVHGEN YETTGEYRVV WQPD GSVFDA AGRG KIGEDV
201 YEHL CLGYQM AQVYLAKYRD VANDEQKVWD FRKESNR IAS DSRNSV FYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKN GNLF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDL SH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

**m728 / g728**

m728.pep	10	20	30	40	50	60
	MFKKFKPVLLSFFALVF AFW LGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVF AFW LGTGIAYEINPRWFLSDTATEVPENPNNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRND RPF SVNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRND RPF SVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPD GSVFDAAGRKGIGEDVYEHCLG CYQMAQVYLAKYRDVANDEQKVWDFR KESNR IAS					
g728	WQPD GSVFDAAGRKGIGEDVYEHCLG CYQMAQVYLAKYRDVANDEQKVWDFR EESNR IAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSV FYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYYLKN GNLF					
g728	DSRDYV FYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYYLKN GNLF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

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```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360
           370
m728.pep  YAEAAAARRSGGRRDLSHX
           |||||
g728      YAEAAAARRSGGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCCAGGTA TATTTGCGCA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCGCGC
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLRYN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKQRQSFYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

a728 / m728 96.3% identity in 377 aa overlap

```

           10      20      30      40      50
a728.pep  MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE--NPNFAFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10      20      30      40      50      60

           60      70      80      90      100     110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV
           |||||
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70      80      90      100     110     120

           120     130     140     150     160     170
a728.pep  WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLRYNDRPFSVNVYGGTVHGENYETTGEYRVV
           |||||
m728      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLRYNDRPFSVNVYGGTVHGENYETTGEYRVV
           130     140     150     160     170     180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSLVVGVDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDLSHX					
m728	YAEAAARRSGGRRDLSHX					
		370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTC TGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCCTCAAT GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTGGGTTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCg
351 caaTGTCAGC AGCAGCTACA ATGTCGGAAT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaaca GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgCGATGCG GCACATTTGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTTGCGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTTCG GCCGTCGCCC TGCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
701 gcCGCGAACA GGCGCGCAAT GCCTTGGAAC CCTTGATTAA ccGTCCGATA
751 CCCGAagaCC TGCCCGCCGG TTTGCCGTTG GACaagcAGT TTTTGTGTTGA
801 AAAACTGCCT GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
851 TCCGCGCGCG CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GGCGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATTT TTACTTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTTGCCTA
1101 TGAATCCGCG GTCCAATCCG CTTTCAAGA CGTGGCAAA GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGATTTGC TCGATGCGGA ACGCATCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDYFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEAAALQ
151 YFASVANRDA AHLILIAIVA KAYFNERYAE KAMSLAQRLV KTREETYKLS

```

```

201  ELRYKAGVIS  AVALRQOEAL  IESAKADYAH  AARSREQARN  ALATLINRPI
251  PEDLPAGLPL  DKQFFVEKLP  AGLSSEVLLD  RPDIRAAEHA  LKQANANIGA
301  ARAAFFPSIR  LTGSGVTGSV  ELGGLFKSGT  GVWAFAPSIT  LPIFTWGTNK
351  ANLDVAKLRQ  QAQIVAYESA  VQSAFQDVAN  ALAAREQLDK  AYDALSKQSR
401  ASKEALRLVG  LRYKHGVSGA  LDLLDAERIS  YSAEGAALSA  QLTRAENLAD
451  LYKALDGGGLK  RDTQTGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2465>:

## m729.seq

```

1   ATGGATACTA  CATTGAAAAC  CACCTTGACT  TCTGTTGCAG  CAGCCTTTGC
51  ATTGTCTGCC  TGCACCATGA  TTCCCAATA  CGAGCAGCCC  AAAGTCGAAG
101 TTGCCGAAAC  GTTCAAAAAC  GATACCGCCG  ACAGCGGCAT  CCGCGCCGTC
151 GATTTAGGTT  GGCATGACTA  TTTTGCCGAC  CCGCGCCTGC  AAAAGCTGAT
201 CGACATCGCA  CTCGAGCGCA  ATACCAGTTT  GCGTACCGCC  GTATTGAACA
251 GCGAAATCTA  CCGCAAACAA  TACATGATTG  AGCGCAACAA  CCTCCTGCCC
301 ACGCTTGCCG  CCAATGCGAA  CGACTCGCGC  CAAGGCAGCT  TGAGCGGCGG
351 CAATGTAAGC  AGCAGCTACA  AAGTCGGACT  GGGTGCGGCA  TCTTACGAAC
401 TCGATCTGTT  CGGGCGTGTA  CGCAGCAGCA  GCGAGGCGGC  ACTGCAAGGC
451 TATTTGCGCA  GCACCGCCAA  CCGCGATGCG  GCACATTGTA  GCCTGATTGC
501 CACCGTTGCC  AAAGCCTATT  TCAACGAACG  TTACGCCGAA  GAAGCGATGT
551 CTTTGGCGCA  ACGTGTTTTG  AAAACGCGCG  AGGAAACCTA  CAAGCTGTCC
601 GAATTACGTT  ACAAGGCAGG  CGTGATTTC  GCCGTCGCCC  TACGTCAGCA
651 GGAAGCCCTG  ATCGAATCTG  CCAAAGCCGA  TTATGCCCAT  GCCGCGCGCA
701 GCCGCGAACA  GGCGCGCAAT  GCCTTGGCAA  CCTTGATTAA  CCAACCGATA
751 CCCGAAGACC  TGCCTGCCGG  TTTGCCGCTG  GACAAGCAGT  TTTTTGTTGA
801 AAAACTGCCG  GCCGGTTTGA  GTTCCGAAGT  ATTGCTCGAC  CGTCCCAGTA
851 TCCGTGCTCG  CGAACACGCG  CTCAAACAGG  CAAACGCCAA  TATCGGTGCG
901 GCACGCGCCG  CCTTTTCC  ATCCATCCGC  CTGACCGGAA  CCGTCGGTAC
951 GGGTTCTGCC  GAATTGGGTG  GGTGTGTTCA  AAGCGGCACG  GGCGTTTGGT
1001 CGTTCGCGCC  GTCTATTACC  CTGCCGATTT  TTACCTGGGG  TACGAACAAG
1051 GCGAACCTTG  ATGTAGCCAA  GCTGCGCCAA  CAGGTACAAA  TCGTTGCCTA
1101 TGAATCCGCC  GTCCAATCCG  CATTTCAAGA  CGTGGCAAAC  GCATTGGCGG
1151 CGCGCGAGCA  GCTGGATAAA  GCCTATGACG  CTTTAAGCAA  ACAAAGCCGC
1201 GCCTCTAAAG  AAGCGTTGCG  CTTGGTCGGC  CTGCGTTACA  AGCACGGCGT
1251 ATCCGGCGCG  CTCGACTTGC  TCGATGCGGA  ACGCAGCAGC  TATGCGGCGG
1301 AGGGTGCGGC  TTTGTGCGCA  CAACTGACCC  GCGCCGAAAA  CCTTGCCGAT
1351 TTGTACAAGG  CACTCGGCGG  CGGATTGAAA  CGGGATACCC  AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2466; ORF 729>:

## m729.pep

```

1   MDTTLKTTLT  SVAAAFALSA  CTMIPQYEQP  KVEVAETFKN  DTADSGIRAV
51  DLGWHDYFAD  PRLQKLIDIA  LERNTSLRTA  VLNSEIYRKQ  YMIERNLLP
101 TLAANANDSR  QGSLSGGNVS  SSKVGLGAA  SYELDLFGRV  RSSSEAALQG
151 YFASTANRDA  AHLSLIATVA  KAYFNERYAE  EAMSLAQRVL  KTREETYKLS
201 ELRYKAGVIS  AVALRQOEAL  IESAKADYAH  AARSREQARN  ALATLINQPI
251 PEDLPAGLPL  DKQFFVEKLP  AGLSSEVLLD  RPDIRAAEHA  LKQANANIGA
301 ARAAFFPSIR  LTGTVGTGSA  ELGGLFKSGT  GVWSFAPSIT  LPIFTWGTNK
351 ANLDVAKLRQ  QVQIVAYESA  VQSAFQDVAN  ALAAREQLDK  AYDALSKQSR
401 ASKEALRLVG  LRYKHGVSGA  LDLLDAERSS  YAAEGAALSA  QLTRAENLAD
451 LYKALGGGLK  RDTQTDK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / g729 95.7% identity in 467 aa overlap

```

              10      20      30      40      50      60
m729.pep      MDTTLKTTLT SVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g729           MNTTLKTTLT SVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD
              10      20      30      40      50      60

```

1179

m729.pep	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
g729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNVS					
	70	80	90	100	110	120
m729.pep	130	140	150	160	170	180
	SSYKVGLGAASYELDLFGRVRSSEALQGYFASTANRDAAHLSLIATVAKAYFNERYAE					
g729	SSYNVGLGAASYELDLFGRVRSNSEALQGYFASVANRDAHLILIATVAKAYFNERYAE					
	130	140	150	160	170	180
m729.pep	190	200	210	220	230	240
	EAMSLAQRVLKTREETYKLSSELYKAGVISAVLRQOEALIESAKADYAHAAARSREQARN					
g729	KAMSLAQRVLKTREETYKLSSELYKAGVISAVLRQOEALIESAKADYAHAAARSREQARN					
	190	200	210	220	230	240
m729.pep	250	260	270	280	290	300
	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
m729.pep	310	320	330	340	350	360
	ARAAFFPSIRLTGTGTGSAELGGLEKSGTGVWSFAPSITLPIFTWGTNKANLQVAKLRQ					
g729	ARAAFFPSIRLTGSGVTGSELGGLEKSGTGVWAFAPSITLPIFTWGTNKANLQVAKLRQ					
	310	320	330	340	350	360
m729.pep	370	380	390	400	410	420
	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
g729	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA					
	370	380	390	400	410	420
m729.pep	430	440	450	460		
	LDLLDAERSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51  ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGC GGTC
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGC GGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTGCGCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGCGCGA ACGTGT TTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTC GCGTGC GCCC TACGTACGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTG GCAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCGCGCGG TTTGCGGTTG GACAAGCAGT TTTTGTGTA
801 GAAGCTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTCC C ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GCGGTTTGGT
1001 TGTTCCGACC TTCCATTACC CTGCCGATTT TTACCTGGGG TACGAACAAG

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1180

```

1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

```

a729.pep
1  MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51  DLGWHDYFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRKY YMIERNNLLP
101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEALQOG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTRRETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSQA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

```

a729 / m729 98.1% identity in 467 aa overlap

	10	20	30	40	50	60
a729.pep	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDYFAD					
m729	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDYFAD					
	10	20	30	40	50	60
a729.pep	PRLQKLIDIALERNLSLRTAVLNSEIYRKYMIERNNLLPTLAANANDSRQGSLSGGNVS					
m729	PRLQKLIDIALERNLSLRTAVLNSEIYRKYMIERNNLLPTLAANANDSRQGSLSGGNVS					
	70	80	90	100	110	120
a729.pep	PRLQKLIDIALERNLSLRTAVLNSEIYRKYMIERNNLLPTLAANANDSRQGSLSGGNVS					
m729	PRLQKLIDIALERNLSLRTAVLNSEIYRKYMIERNNLLPTLAANANDSRQGSLSGGNVS					
	70	80	90	100	110	120
a729.pep	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVA KAYFNERYAE					
m729	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVA KAYFNERYAE					
	130	140	150	160	170	180
a729.pep	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVA KAYFNERYAE					
m729	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVA KAYFNERYAE					
	130	140	150	160	170	180
a729.pep	EAMSLAQRVLKTRRETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
m729	EAMSLAQRVLKTRRETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
	190	200	210	220	230	240
a729.pep	EAMSLAQRVLKTRRETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
m729	EAMSLAQRVLKTRRETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
	190	200	210	220	230	240
a729.pep	ALATLINQPI PDDLPAGLPLDKQFFVEKLP AGLSSEVLLD RPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PDDLPAGLPLDKQFFVEKLP AGLSSEVLLD RPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
a729.pep	ALATLINQPI PDDLPAGLPLDKQFFVEKLP AGLSSEVLLD RPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PDDLPAGLPLDKQFFVEKLP AGLSSEVLLD RPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
a729.pep	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ					
m729	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ					
	310	320	330	340	350	360
a729.pep	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ					
m729	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK ANLDVAKLRQ					
	310	320	330	340	350	360
a729.pep	QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR ASKEALRLVGLRYKHGVSQA					
m729	QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR ASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420
a729.pep	QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR ASKEALRLVGLRYKHGVSQA					
m729	QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR ASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420



1181

	430	440	450	460
a729.pep	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
m729	LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

1	GTGAAACCGC	TGCGCAGACT	GACAAACCTC	CTTGCCGCCT	GCGCCGTAGC
51	GGCGGTCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	GCGCAAGACC
101	CGTTCATTAC	CGATAACACC	CAACGGCAGC	ACTACGAACC	CGCGGGCAAA
151	TACCACCTCT	TCGGCGaCCC	GCGCGGCAGC	GTTTCCGACC	GCACCGGCAA
201	AATCAACGTC	ATCCAAGACT	ATACCCACCA	GATGGGCAAC	CTGTCATCC
251	AACAGGCGGC	AATCCAAGGC	AATCTTGGTT	ACACCGTCCG	CTTTTCCGGA
301	CACGGACACG	AAGAACACGC	CCCCTTCGAC	AACCACGCCG	CCGACAGCGC
351	AAGCGAAGAA	AAAGGCAACG	TTGACGACGG	CTTTACCGTG	TACCGGCTCA
401	ACTGGGAAGG	ACACGAACAT	CATCCC GCCG	ATGCCTACGA	CGGCCCGAAG
451	GGCGGCAATT	ACCCCAAAACC	TACGGGCGCA	CGAGACGAAT	ACACCTATCA
501	CGTCAACGGC	ACAGCCCCGA	GTATCAAAC	CAATCCGACC	GACACCCGCA
551	GCATCCGGCA	ACGCATATTC	GACAAC TACA	ACAACCTCGG	CAGCAATTTT
601	TCCGACCGCG	CCGATGAAGC	CAACAGAAAA	ATGTTGAGC	ACAATGCCAA
651	GCTCGACCGC	TGGGGCAACA	GCATGGAGTT	TGTCAACGGC	GTCGCCGCCG
701	GCGCGCTCAA	CCCCTTTATC	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC
751	ATACTGTACG	GAACGCGCTA	TGCCATAGAC	AAAGCCGCGA	TGCGCAACAT
801	CGCCCCCTTA	CCCGCCGAGG	GCAAATTTCG	CGCCATCGGC	GGCTTGGGCA
851	GCGCGGCGGG	CTTTGAAAAA	AATACGCGCG	AAGCCGTTGA	CCGGTGGATA
901	CAGGAAAACC	CCAATGCCGC	CGAAACCGTC	GAAGCCCTGG	TCAACGTCCT
951	GCCGTTTGCC	AAAGTCAAAA	ACCTGACAAA	GGCGGCAAAA	CCGGGGAAGG
1001	CTGCGGTTAG	TGGGGATTTT	TCTAAATCCT	ACACCTGCTC	CTTCCACGGC
1051	AGCACCTTGG	TCAAAACGGC	AGACGGCTAC	AAAGCCATTG	CCCATATTCA
1101	AGCCGGAGAC	CGCGTCCCTT	CCAAGGACGA	GGCAAGCGGA	GAAACGGGAT
1151	ACAAACCCGT	TACCGCCCGA	TACGGCAATC	CGTATCAAGA	AACCGTTTAC
1201	ATTGAAGTTT	CAGACGGCAT	CGGCAACAGC	CAAACCCTGA	TTTCCAACCG
1251	ATCCACCCG	TTTTATTTCG	ACGGCAAATG	GATTAAGGCG	GAAGATTTAA
1301	AAGCGGGAAG	CCGGCTGTTA	TCCGAAAGCG	GCAAAACCCA	AACCGTCCGC
1351	AACATCGTTG	TCAAACCAAA	ACCGCTCAA	GCCTACAATC	TGACCGTTGC
1401	CGATTGGCAT	ACCTACTTCG	TCAAGGGTAA	TCAGGCGGAA	ACGGAAGGGG
1451	TTTGGGTTCA	TAATGATTGT	CCGCCTAAAC	CAAAACCAAC	CAATCATGCC
1501	CAACAAAGAA	AAGAAGAAGC	TAAAAACGAT	TCTCATCGAA	GTGTGGGAGA
1551	TTCCAATCGT	GTCGTTTCGCG	AAGGAAAGCA	ATATTTAGAT	TCCGACACAG
1601	GAAACCATGT	TTATGTAAAA	GGAGATAAAG	TGGTTATTCT	AACTCCTGAT
1651	GGAAGACAGG	TAAC TCAATT	TAAGAACTCG	AAAGCCAATA	CGTCAAAAAG
1701	GGTAAAAAAT	GGGAAATGGA	CACCAAAATA	A	

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

1	VKPLRRLTNL	LAACAVAAVA	LIQPALAADL	AQDPFITDNT	QRQHYEPGGK
51	YHLFGDPRGS	VSDRTGKINV	IQDYTHQMGN	LLIQQAAIQG	NLGYTVRFSG
101	HGHEEHAPFD	NHAADSASEE	KGNVDDGFTV	YRLNWEHGEH	HPADAYDGP
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIF	DNYNNLGSNF
201	SDRADEANRK	MFEHNAKLDR	WGNSMEFVNG	VAAGALNPFI	SAGEALGIGD
251	ILYGTRYAID	KAAMRNIAPL	PAEGKFAAIG	GLGSAAGFEK	NTREAVDRWI
301	QENPNAAE TV	EALVNVLPFA	KVKNLT KAAK	PGKAAVSGDF	SKSYTCSFHG
351	STLVKTADGY	KAI AH IQAGD	RVLSKDEASG	ETGYKPV TAR	YGNPYQETVY
401	IEVSDGIGNS	QTLISNRIHP	FYSDGKW IKA	EDLKAGSRL	SESGKTQTVR
451	NIVVKPKPLK	AYNLT VADWH	TYFVKGNQAE	TEGVVWHNDC	PPKPKPTNHA
501	QQRKEEAKND	SHRSVGD SNR	VVREGKQYLD	SDTGNHVYVK	GDKVVILTPD
551	GRQVTQFKNS	KANTSKRVKN	GKWTPK*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

1	GTGAAACCGC	TGCGCAGACT	GACAAACCTC	CTTGCCGCCT	GCGCCGTAGC
51	GGCGGCCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	GCGCAAGACC

1182

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101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GGCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAACCT CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAA GCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAA TTAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1 VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51 YHLFGDPRGS VSDRTGKINV IQDYTHOMGN LLIQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEHGEH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADANRKM FEFHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFNLQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

          10      20      30      40      50      60
g730.pep  VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VKPLRRLTNLLAACAVAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS
          10      20      30      40      50      60

          70      80      90      100     110     120
g730.pep  VSDRTGKINVIQDYTHQMGNLLIQQAIIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE
          70      80      90      100     110     120

          130     140     150     160     170     180
g730.pep  KGNVDDGFTVYRLNWEHGEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      KGNVDEGFTVYRLNWEHGEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT
          130     140     150     160     170     180

          190     200     210     220     230     240
g730.pep  DTRSIRQRIFDNNYNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFVNGVAAGALNPFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNMSEFINGVAAGALNPFI
          190     200     210     220     230     240

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1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAKAALPGKAAVSGDFSYSYTCFSHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAAAQKAKLAKAALPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVRTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNPNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TCGGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GGCGGCCGCA  CTCATACAGC  CCGCCCTCGC  GGCGGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTTCGGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCCTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GGCGGCAATT  ACCCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCCGCCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCGCAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTTCG  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTTGA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 CCGGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAACCTAG
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACAGGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCT
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCTGATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACGT
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRRLIKL  LAACAVAAAA  LIOPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNMSEFING  VAAGALNPF  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSVAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAKAAL  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQNQKNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFPGK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARWV  SYETRDGIRI  RTVYEPATGK  VVTAFDPRTS  NPKYNPVK*

```

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRLRIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730.pep	DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNSEFINGVAAGALNPFI					
m730	DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNSEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPAFAVKVNLTKAAKPGKAAVSGDFSAAYNTRTTTRKVTTEGLN					
m730	QENPNAAETVEAVFNVAATAKAKLAKAAKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNIHINVLSGNSIQHILYGDEAGGGHLPFGKPGKTTTFQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gatttttcgag cgttttcatG CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC
101 TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTCGGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2476; ORF 731.ng&gt;:

```

g731.pep
1  DFRAFSCENG LSVRVRLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA GGTTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGCGGCG
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCCTGCGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG

```

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```

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
301 CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

```

m731.pep
  1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
  51 NGLSVRVRL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

g731/m731 95.2% identity in 84 aa overlap

```

                                10      20      30
g731.pep                      DFRAFSCENGLSVRVRLDGGKIALRLDGR
                                |||:|||||:|||||:|||||:|||||
m731      LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRLDSGKVALRLDGR
              20      30      40      50      60      70

                                40      50      60      70      80
g731.pep      RAVLSSDVAAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m731      RAVLSSDVAAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX
              80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

```

a731.seq
  1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTTGGCGGC
  51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

```

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

```

a731.pep
  1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
  51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

```

a731/m731 94.4% identity in 126 aa overlap

```

                                10      20      30      40      50      60
a731.pep      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRAFSCENGLSVHVRRL
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m731      MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRL
              10      20      30      40      50      60

                                70      80      90      100     110     120
a731.pep      DGGRIALRLDGRRAVLSSDVAAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE
              |:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m731      DSGKVALRLDGRRAVLSSDVAAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE
              70      80      90      100     110     120

a731.pep      TSCRARX
              |||||
m731      TSCRARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

```

g732.seq
  1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
  51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtC CTGCCGTGTC AATCCATCCG TACGATGGCG

```

```

151 GAGGTTTACG GTCAGATTAA GGCAAACACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCCTGCCG AGTTGAAAAC GATTCCGATG ACGgtATTGG TcaaTTCCGG
951 TTCggttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTACGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCTtgcCGTA CCGCTTGAAG AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGTT TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

**g732 . pep**

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRDNEV LPVQSIRTMA
51 EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YGMGGDPLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGKSVQT
351 LIPLNSGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

**m732 . seq**

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAAGCGT AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCATTCTCTG AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGAGA TTGTCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GCGCGATTGT
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

**m732.pep**

```

1  MSKPVFVKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLGA
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLNSGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKDADKPA VKEKGKKKDD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKDKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

**m732/g732** 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFVKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEYVGQIKANY					
g732	MSKPVFVKIALYTLGAISGVAVSLAVQGFAAEKDGRDNEVLPVQSIRTMAEYVGQIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	:					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m732.pep	VSPIDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
g732	VSPIDTPAERA EVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLGA					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m732.pep	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
g732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLNSGSAV					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
g732	PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVS NKDKKDKKDKKX					
g732	PVS NKDKKDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTGTCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAC CATAACGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTGCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTTCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGC GGATTG
1201 GTCGGACACA TCGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCGCCAAAAG ACGACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YGMGDSLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGVSQVT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVS NKDKKDK KDKK*

```



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a732/m732 99.6% identity in 494 aa overlap

	10	20	30	40	50	60
a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGQIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGQIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
a732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
a732.pep	LDLRDDPGGLLTGAVGVSA AFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG					
m732	LDLRDDPGGLLTGAVGVSA AFLPSEAVVVSTKGRDGKDRMVLKAI PEDYVYGMGGDSLAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
a732.pep	IPAELKTIPMTVLVNSGSASASEIVAGALQD HKRAVIVGTQSFGKGSVQT LIPLSNGSAV					
m732	IPAELKTIPMTVLVNSGSASASEIVAGALQD HKRAVIVGTQSFGKGSVQT LIPLSNGSAV					
	310	320	330	340	350	360
	370	380	390	400	410	420
a732.pep	KLTTALYYTPNDRS IQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTPNDRS IQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
a732.pep	PLEKDADKPAVKEKGKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
m732	PLEKDADKPAVKEKGKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
a732.pep	PVS NKDKKDKKDKKX					
m732	PVS NKDKKDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGa cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCC CGGGTGC GCA CGCCATTG GGA CTGCTG C

```

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251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

**g733.pep**

1 MMNPCTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS  
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE  
 101 KRLFPESGVF MDFLMKTGKG GKR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

**m733.seq**

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG  
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA  
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC  
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

**m733.pep**

1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS  
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE  
 101 KRLFPESGVF MDFLMKTGKG GKR\*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

**m733/g733**

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
g733	MMNPCTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
g733	YFAEAANKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
g733	YFAEAANKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
m733.pep	GKRX					
g733						
	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

**a733.seq**

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG  
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA  
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC  
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

**a733.pep**

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```

1  MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              |||
m733          MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              |||
m733          YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              |||
m733          GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCGGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGGCC TTTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATGCACGT CATCTCTTA TTACGGCGGG
451 GCTGTTCGCT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2494; ORF 734.ng&gt;:

```

g734.pep
1  MMKKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKQDITLAG IAEDPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKYG AQQQCGLETV YCTSSSYYG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCCG TCGTGTGCTG
51  GAACAATACC TGTGTCGCGC TGGCATAACC GAAAGCCTTG GGCGCGCTGC
101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCAAGT CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGAA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACTG
251 TCGGCTCTTT GATTCAAAAT CTCAATAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2496; ORF 734&gt;:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSVLNNT CVALAYPKAL GALRVDNAVV ITSPRFTSVH
51  QVALNQCIKK YGVQGCGLT TVYCTSSSY GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEDEPTGCRSVSVLNNTCVALAYPKAL
              :|||
g734          VLQVKTTKEDSAKSEAFAELEAFCKQDITLAGIAEDEPTGCRSVSVLNNTCVSLAYPKAL

```

	40	50	60	70	80	90
m734.pep	GALRVDNAVVTISPRFTSVHQVALNQCIKKYGVQGQCGL	ETVYCTSSSYYG	TVRSLIQN			
g734	GAMRVENAVVTISPRFTSVHQVALNQCIKKYGAQGCGL	ETVYCTSSSYYG	GA VRSLIQH			
	100	110	120	130	140	150
m734.pep	LKX					
g734	LKX					
	160					

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTG CAGGTAAAAA CCACAAAAGA AGATTGCAGC
151 AAAAGCGAAG CGTTTGCCGA GTTGGAAGCT TTCTGCAAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG AGGAGCCGAC CGGATGCCGG TCGGTCTGTG
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAACAACGT TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCTCAAA TAA
```

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVW	QNPQNANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSINNTCV	ALAYPKALGA
101	MRVENAVVIT	SPRFTSVYQV	ALNQCIKKYG	AQGQCGLETV	YCTSSSYGG
151	TVRSILONLK	*			

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVLAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
	130	140	150	160		
a734.pep	ALNQCIKKYGAQGQCGLETVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGQCGLETVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		

m735.seq	1	ATGAATCTCG	TGAAACTGCT	GGCGAATAAC	TGGCAACCGA	TTGCCATTAT
	51	CGCGCTTGTC	GGCACGGGCT	TGGCTGTGTC	GCACCATCAA	GGCTACAAGT
	101	CGGCATTGTC	GAAGCAGCAG	CGGCTCATCG	ACAAGATGGA	CGCGCAACAG
	151	GCGCAAGCCC	TGCTGTTGTC	GGCTCAAAC	TATGCGCGCG	AACTGGAACT
	201	GGCACGCGCG	GAAGCTAAAA	AATATGAAGT	CAAGGCGCAC	GCTGTCGGGA
	251	TGGCTTTGGC	GAAAAAACAG	CGGGAAGTCA	GCCGCTGTA	AACGGAAAAA
	301	AAAAAGGAAA	TCGAAATGT	CCTTAECTAA	GACCGTAAAA	ATGCAGCGCG

m735.pcp

a735.seq

a735.pcp

a735/m735 95.7% identity in 139 aa overlap

**g736.seq**

1	ATGAATTTTA	TCCGTTCCGT	CGGGGCGAAA	ACCCCTCGGC	TTATTCAATC
51	CTTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	CATTTTGCGG	AAATCCGGCA
101	CGGCTTTCGC	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTTGCCGGC
151	GTGCTGTGCG	TGCTGATTGT	TGCCGTTTCG	GGGCTGTTCG	TCGGTATGGT
201	TTTGGGTTTG	CAGGGCTATA	CGCAGTTGTC	GAATTCCAA	TCGCCCGATA
251	TTTTGGGCTA	TATGGTCCGC	GCTTCTCTGT	TGCGCGAACT	GGGTCCCGTG
301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA
351	AATCGGTTTG	ATGAAAACGA	CCGGACAGCT	CGAAGCGATG	AACGTGATGG
401	CGGTC AACCC	CGTCGCCCGC	GTGGTTGCCC	CGCGTTTTTG	GGCGGGCGTG
451	TTTTCTATGC	CGCTTTTGGC	TTGCATTTTC	AACGTCGCGG	GCATTTTTCG
501	CGCGTATTTG	GTCGGCGTGA	GCTGGCTGGG	TTTGACACAG	GATTATTTCT
551	GGCCGCAGAT	GCAGAACAAAC	ATTACGATAC	ATTACGATGT	AATCAACGGT

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```

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

**g736.pep**

```

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG
51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVG
201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

**m736.seq**

```

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCCGCAGT ATCACGCTGT TTCTGCTGAA CATTGTGGCG AAATCCGGCA
101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGCG
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATCAAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGGAACT GGGTCCCCTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GGCGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT
601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

**m736.pep**

```

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDVG
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

**m736/g736**

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
g736	MKTTGQLEAMNMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVIINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
g736	GIFWPQMNNITIHYDVIINGLIKSAAFGVAVTLIAVHQGFHCIPPTSEGILRASTRTVVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

```

a736.seq
1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCACGCTGT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCCG TGTGATTGT TGCCGTTTCA GGGCTGTTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TGCGCGAACT GGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGCGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGGCGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTTG GTCGGTGTA CCTGGCTGGG CTTGGACAGC GGTATTTTCT
551 GGTCGCAAAAT GCAGAACAAAC ATCACGATAC ATTACGATGT AATCAACGGT
601 CTGATCAAAAT CCGCCGCGTT CGGCGTGCGG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCCT GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

```

a736.pep
1  MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDVIING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
m736	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVIINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

1196

```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep  ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

**g737.seq**

```

1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

**g737.pep**

```

1  MNIKHL LTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKA AWAR VGGKITDIDL EHD DGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

**m737.seq..**

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCAGC GTTGGGCGGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

**m737.pep**

```

1  MNIKHL LLS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKA ALAR VGGKITDIDL EHD NGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

**m737/g737**

```

           10      20      30      40      50      60
m737.pep  MNIKHL LLSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQA EKAALAR
           |||||:|||||:|||||:|||||:|||||:|||||
g737      MNIKHL LLAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISRQA EKA AWAR
           10      20      30      40      50      60

           70      80      90      100      109
m737.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||:|||||:|||||:|||||:|||||:|||||
g737      VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:



1197

a737.seq  
 1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG  
 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC  
 101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC  
 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG  
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG  
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC  
 301 GTGATTTCTT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep  
 1 MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR  
 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR  
 101 VISSRRDD\*

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTAAAT	ALMGISAPALAHHDGHG	DDDHGHAHQHSKQDKIISR	AQAEKAALAR		
m737	MNIKHLLLTSAAT	ALLSISAPALAHHDGHG	DDDHGHAHQHNKQDKIISR	AQAEKAALAR		
	10	20	30	40	50	60

  

	70	80	90	100	109
a737.pep	VGGKITDIDLEHDNGRPHYD	VEIVKNGQEYKVVVDARTGR	VISSRRDDX		
m737	VGGKITDIDLEHDNGRPHYD	VEIVKNGQEYKVVVDARTGR	VISSRRDDX		
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq  
 1 ATGTCGGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCCG CCAAACCTGCC  
 51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT  
 101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCCGCGCC  
 151 GCGGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT  
 201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT  
 251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC  
 301 GACATCGCCT CTGGGTTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG  
 351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtT ACCCTGTTTG  
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC  
 451 CAGTTTGCCG GCTGGGAAAA CACCCCCCTG CTTCAAAACA TCATCGTTCA  
 501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC  
 551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CTAACCTCAA CGGACAACGA  
 601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT  
 651 TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG  
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG  
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT  
 801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG  
 851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC  
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA  
 951 CGGCTGGAAC AGTTTGTCCC AACAAACCTT CCTGATCAAT GCCGAACAGC  
 1001 ACACCATACA CGACAACCTT CTCAGCACCT TGTTCAACCA TTCCCAAC  
 1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT  
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA  
 1151 CCCCCGCATC ACTTTTCCTG CTGTGCGCGC TTGCCGTGAG TATGTGCCAC  
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG  
 1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA  
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCGA  
 1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC  
 1401 CCCC GCCGCT GACGACAGTG CAAAACCTT CAACCGGAAA ATCAACGAAC  
 1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCCTTTTA TGCCGACTTC  
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC  
 1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCTAC TCCGCCACCT

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1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

**g738.pep**

```

1  MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51  AAGLIVLLFL TAGKKLFDVK IPAISFLLEA MAAFWWLQAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFOFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHWN SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGL IAFKKAANLG ILTASAAIFA
451 GLLHLDWTYT RLVSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEBA TLKALKYRPY SATYRIALYL MRQKVAEAK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

**m738.seq**

```

1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCG
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAAA ATCCCGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGCGCT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG CTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCTCATCCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCGAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTTGCC AACAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTTCA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

**m738.pep**

```

1  MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

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1199

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51  AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILEFTTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

**m738/g738**

m738.pep	10	20	30	40	50	60
	MPAETTIVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTIVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
	TAGKKLFDVKIPAISFLLFAMAFAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIPAISFLLFAMAFAFWYLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
	VAHFGQERIVTFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
	NLGHYLMWGI LAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWGI LAAAYLNGQRKIPAAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
	YFRSDKSNRRTMLGIAAAVFLTALFQFSMN TILEFTTGIRYETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRRTMLGIAAAVFLTALFQFSMN TALEFTTGIRYETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHNIYDNL LSNLFTHSHNIVLQLLAEMG					
g738	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHTIHDNLFSTLFTTHSHNII LQLLAEMG					
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	ISGTLLVAATLLTGIAGLLKRSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
	FLSPAESDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
g738	FLSPAESDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNSFSPAADDDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKALKYRPPSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCCKX					
g738	KPCCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738.seq
1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAAC TGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGCCG TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATTGTTTA
501 CAGCGGGCAA GCGGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CCGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCAACCA TTCCCAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTCG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACC GCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGA CTGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAC TGCCCGTATG GCGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738.pep
1  MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALRLQP SPDFYHDA
51  AAGLIVLFL TAGKKLFDVK IPPISFLLFA MAAFYWLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```

1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR  
251 TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI  
301 EWRKALAAEQ SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTHSHN  
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH  
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAAIFA  
451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF  
501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK  
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHEA  
601 KPCK\*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
a738.pep	TAGKKLFDVKIPPIISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
m738	TAGKKLFDVKIPAIISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a738.pep	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a738.pep	NLGHYLMWGILAAAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
a738.pep	YFRSDKSNRRITILGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
m738	YFRSDKSNRRITMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a738.pep	EWRKALAAEQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
m738	EWKALAAEQSAPIFGHGWN SFAQQTFLINAEQHNIDNL LSNLFTHSHNIVLQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a738.pep	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
a738.pep	FLSPAESDGI IAFKKAANLG ILTASAAI FAGLLHLDWYTYRMVNAFSPATDDSAKTLNRK					
m738	FLSPAESDGI IAFKKAANLG ILTASAAI FAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
	490	500	510	520	530	540
a738.pep	INELRYISANSPMLSFYADFSLVNFALEPY PETQTWAEATLKSLKYRPHSATYRIALYL					
m738	INELRYISANSPMLSFYADFSLVNFALEPY PETQTWAEATLKSLKYRPHSATYRIALYL					
	490	500	510	520	530	540

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	550	560	570	580	590	600
a738.pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
m738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600
a738.pep	KPCKX					
m738	KPCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

**g739.seq**

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGG CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

**g739.pep**

```

1  MAKKPNKPF R LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAO PKETPKKET PKENHTKPD T PKNTPAKPHK EILDNLFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

**m739.seq**

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAGA
501 AAACCATACC AAACCGGACA CCCCAGAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

**m739.pep**

```

1  MAKKPNKPF R LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAO PKETPKENHT KPDTPKNTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

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	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAVGIVSTFNPNGDKTLQAEPOHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSPAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPHKEILDKLF					
g739	PKNTPAKPHKEILDNLF					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1   ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCTCGTA CTGCCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCATATAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1   MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSLP
101 SPAAPKKNRV KPQPADTAQT DRQPDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPDTPKNTPPKPHK EILDNLF*

```

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPOHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAVGIVSTFNPNGDKTLQAEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
m739	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

                190
a739.pep      PKNTPPKPHKEILDNLFX
                |||||
m739          PKNTPPKPHKEILDKLF
                180      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTGCGCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATTt
201 GAAACgtcaa ACCATGTTTC TGTTTATTCC GATTGTTTTG CTGGTTGTGT
251 ATTTGTTCCA CTATTTCCGC GCGTTTTag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHLLINGII LACEATFLFK
51 FVLFDTIKHH LKQGFDLKRQ TMLLFIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCTCCAGC
101 ATCTGATCAA CGGCATCATC CTGCGCTGCG AAGCGACGTT TTTGTTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTt
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLLINGII LACEATFLFK FVLFDTIKHH
                |||||
g740          MSRNLLVRWLA VCLIPLATL AVFAANPPED KPQHLLINGII LACEATFLFK FVLFDTIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPIIL LIVYLFHYFG AFX
                |||
g740          LKQGFDLKRQ TMLLFIPIVL LVVYLFHYFG AFX
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTGCGCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTt
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHLLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

                10      20      30      40      50      60

```



1205

```

a740.pep      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
|||||||:|||||||
m740          MSRNLLVRWLVAVCLIPLATLAVFAANPPEDKLQHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep      LKQEFDLKRQTMLLFIPILLIVYLFHYFGAFX
|||||||
m740          LKQEFDLKRQTMLLFIPILLIVYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGCGGGAGG CGGTGGTGTC GCCGCGGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAAACCTG ACCTATACCA TAGATTTGCG CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCCTCCGC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAEKTFK AGGKDNSLNT GLKNDKISR
101 FDFVQKIEVD GQTITLASGE FQYKQDHSV VVALRIEKIN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 HLGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCGGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGTTTGT
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCGACAA GGTGCGGAAA AAACCTTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GCGGACATAG CCGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGAT GGAACGCGC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRLFDFIRO
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMKVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYYTID FAAKQGNNGKI  
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA  
 251 QEVAGSAEVK TVNGIRHIGL AAKQ\*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCSLT---	ALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQ			
g741	VNRTTFCCSLTAGPDS	DRLQRRGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEA			
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAQA	EKTY---GNGDSLNTGKLKNDKVS	RFD	FIRQIEVDGQLITLES	GE
g741	SIPQNGTLTLSAQ	EKTFKAGGKDNSLNTGKLKNDKIS	RFD	VFQKIEVDGQTITLAS	GE
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAF	QTEQIQDSEHSGKMKVAKRQFRIG	DIAGEHTSF	DKLPEGGRATYRGT	
g741	FQIYKQDHSAVVAL	RIEINNPKIDSLINQSRFLVSD	LGEHTAFNQLPDG	-KAEYHKG	
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLT	YIDFAAKQGNNGKIEHLKSP	ELNVDLAAADIKPD	GKRHAVISGS	VLYN
g741	AFSSDDADGKLT	YIDFAAKQGHGKIEHLKTP	EQNVELASAE	LKADEKSHAVIL	GDTRYG
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYS	SLGIFGGKAQEVAGSAEVK	TVNGIRHIGL	AAKQX	
g741	GEEKGTYRLAL	FGDRAQEIAGSATVKIG	KEVHEIGI	ADKQX	
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq  
 1 GTGAACCGAA CTGCCTTCTG CTGCCTTTCT TTGACCGCCG CCCTGATTCT  
 51 GACCGCCTGC AGCAGCGGAG GCGGCGGTGT CGCCGCCGAC ATCGGCGCGG  
 101 TGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAAGTTTG  
 151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAACGAGA AACTGAAGCT  
 201 GCGGCGACAA GGTGCGGAAA AAACCTATGG AACCGCGAC AGCCTCAATA  
 251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAA  
 301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGCGGAG AGTTCCAAGT  
 351 GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC  
 401 AAGATTCCGA GCATTACGGG AAGATGCTTG CGAAACGCCA GTTCAGAATC  
 451 GCGGATATAG CGGGTGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG  
 501 CAGGGCGACA TATCGCGGGA CGGCATTCCG TTCAGACGAT GCCAGTGGAA  
 551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGACA CGGCAAAATC  
 601 GAACATTGTA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT  
 651 CAAGCCGGAT AAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA  
 701 ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC  
 751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAACG GCATACGCCA  
 801 TATCGGTCTT GCCGCCAAGC AGTAA

This corresponds to the amino acid sequence &lt;SEQ ID 2538; ORF 741.a&gt;:

a741.pep  
 1 VNRTAFCCLS LTAALILTAC SSGGGGVAAD IGAVLADALT APLDHKDKSL  
 51 QSLTLDQSVR KNEKLKLAQA GAETYGNGD SLNTGKLKND KVSFRDFIRQ  
 101 IEVDGQLITL ESGEFQVYKQ SHSALTALQT EQVQDSEHSG KMKVAKRQFRI  
 151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD ASGKLTYYTID FAAKQGHGKI  
 201 EHLKSPELNV DLAAADIKPD KKRHAVISGS VLYNQAEKGS YSLGIFGGQA  
 251 QEVAGSAEVE TANGIRHIGL AAKQ\*

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDIFRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDIFRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYTIDFAAKQGHGKIEHLKSPELNVDLAASDIKPDKKRHAVISGSVLYNQAEKGS					
m741	AGGKLTYTIDFAAKQGNKGKIEHLKSPELNVDLAAADIKPDKKRHAVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAAKQX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAAKQX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

```

m742.seq
1   ATGGTTTACG GCATTGCCGA AGCCGATGCG GCGACAGCA GTGTGCTTAC
51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGCC CTGTGAAAAT CAGAAACTG CCCCCTTCAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTAAGTGCCG ACAAATACAA CCTTTTCTCA GGATTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAATATGC
351 GGCGGGTTTG TCGGGTGAGG ATGCGGTAGG CTTTTTGACT GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGATG AAACCGCCAA GGAATACCGG GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTTCG ACAGTATCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACAAGT GTATGAGTGA CCCTTTCGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGCG TTGATGCCGA
651 CAAGGCGGAA TTTGTGCGTA AAGCCCTTGC GAAGGAGGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTTCGGCG GGAGCATGAT TTCTTTGTCG GCTATGCCTA CGGTGATGAA
901 AAGATACGTT CGGAATATCT AGAAATCTAC GAACGCCGCT ACAGAGTACG
951 TCCGAATACG GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAAGAGG
1001 AGCCGGACGG CGATTTGTCG TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAC GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACACCGGTA
1201 TATGTCGATG TATATGAGCT GGACGAAAAA GGCAACAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCTG CCTTTACCGG TTTTTCGGT ACGGTGCCGG
1301 TTTGAAAAAC CGTCAAAGTG GCAGACGACC ATGTTCTTGC GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAACC CATTGCTGTA CTGCCAGCAC
1401 GCGTTTCAAC GTAACGGGCC GACTGCACCT TTTGGGCGGG CTGCACTACA

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1208

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1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACATAG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTGCTCG ATTTTCGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCGGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
1  MUYGIAEADA GDSSVLTGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAERKAG FDKCMSDPFA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAAQRF NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FFGYAYGDE
301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEP DGDLS SPLVRGHKEP
351 DWQAYDEKGN RTVYAEERN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWTKVKV ADDHVPALYN
451 YAKYLNNTKT HSLTASTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRITYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
1  ATGGTTTACG GCATTGCCGA AGCCGATGCG GCGACAGCA GTGTGCTTAC
51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTCCTGAT TTTTCGGGCA
101 TTATTTTGTC CTGTGAAAAT CAGAAACTG CCCGTTTACG TTCAACGCCA
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
351 GCGGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTTCA GCAGTACCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTGCGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTGCGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGCGGATGAA
901 AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAGGGGG
1001 AGCCGGACGG TGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAAACCGA GCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

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a742.pep
1  MVGIAEADA GDSSVLTLGG MYQKSREVPD FSGIILSCEN QKTAPFSSPT
51  ACNRPLQLPR NTYLGEDHWR LSADKYNLFS GFKHVFDNGW QLNAEVSYTK
101 NESDAQVQGF FLKNEHWAAGL SDEDAVGFLT EKNEVIPFEP KDKALEKLLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDECMSAPFA
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAQRFEP NSLYDSSFN
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FVGVYAGDE
301 KIRSEYLEIY ERRHRVRPNT GATHGVYAGS CQGEPDGDL SFLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVFVWKTVKV ADDHVPALYN
451 YAKYLNNTKT HSLTAGTRFN VTGRLHLLGG LHYTRYETSP TKDMPVRYQG
501 PASDFQNTAS IKADQDHYTA KMQGHKLTPQ AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRLNASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKGSRYN AAEVNAERLA KNTGADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RSTRGANNFYG EPRTVSMKLD WOF*
```

	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSSVLT	LGGMYQKSREVP	DFSGIILSCENQKT	APFSSTPACNRPL	QLQPR	
m742	MVYGIAEADAGDSSVLT	LGGMYQKSREVP	DFSGIILPCENQKT	APFSSTPACNRPL	QLQPR	
	10	20	30	40	50	60
	70	80	90	100	110	120
a742.pep	NTYLGEDWSRLSADKYN	LFSGFKHVF	DNGWQLNAEVSYTKNES	DAKVGVQFFL	KNEHAAGL	
m742	NTYLGEDWSRLSADKYN	LFSGFKHVF	DNGWQLNAEVSYTKNES	DAKVGVQFFL	KNEYAAGL	
	70	80	90	100	110	120
	130	140	150	160	170	180
a742.pep	SDEDAVGFLTEKNEVIP	FEFKDKALEKLKAYR	DETAKEYRERKDDFV	KNRFDNTAFEQYR		
m742	SGEDAVGFLTEKNEVIP	FEFKDKALEKLKAYR	DETAKEYRERKDDFV	KNRFDNTAFEQYR		
	130	140	150	160	170	180
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDECM	SAPFALDFICOGS	WDPGVDADKSEFV	DKALAKEGIFNNA	AORF	

1210

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|||||:|||||:|||||
m742  SRRAAERKAGFDKCMSDPFALDFICQSSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
      190      200      210      220      230      240
      250      260      270      280      290      300
a742.pep NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKLDLTGTYGLFGREHDFVGYAYGDE
|||||
m742  NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKLDLTGTYGLFGREHDFVGYAYGDE
      250      260      270      280      290      300
      310      320      330      340      350      360
a742.pep KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEFPGDLSSPLVRGHKEPDWQAYDEKGN
|||||:|||||
m742  KIRSEYLEIYERRYVRPNTGATHGVYAGSCQEEFPGDLSSPLVRGHKEPDWQAYDEKGN
      310      320      330      340      350      360
      370      380      390      400      410      420
a742.pep RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQTNP
|||||
m742  RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQTNP
      370      380      390      400      410      420
      430      440      450      460      470      480
a742.pep GTPAFTGFSGTVPVWKTVKVADDHVPALYNYAKYLNTNKTSLTAGTRFNVTGRLHLLGG
|||||:|||||
m742  GTPAFTGFSGTVPVWKTVKVADDHVPALYNYAKYLNTNKTSLTAGTRFNVTGRLHLLGG
      430      440      450      460      470      480
      490      500      510      520      530      540
a742.pep LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQ
|||||:|||||
m742  LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTPYAGITYDLTPQ
      490      500      510      520      530      540
      550      560      570      580      590      600
a742.pep QSIYGSYTKIFKQQDNVDVSAKTVLPLVGTNYEVGWKGAFLOGLNASFALFYLEQKNR
|||||
m742  QSIYGSYTKIFKQQDNVDVSAKTVLPLVGTNYEVGWKGAFLOGLNASFALFYLEQKNR
      550      560      570      580      590      600
      610      620      630      640      650      660
a742.pep TVVDFGYVPGAGGKQGSFQTVAKPIGVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKN
|||||
m742  TVVDFGYVPGAGGKQGSFQTVAKPIGVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKN
      610      620      630      640      650      660
      670      680      690      700      710      720
a742.pep AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
|||||:|||||
m742  AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
      670      680      690      700      710      720
      730      740      750      760      770      780
a742.pep RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
|||||
m742  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
      730      740      750      760      770      780
a742.pep WQFX
      ||||
m742  WQFX
```

a742/ p25184

sp|P25184|PUPA\_PSEPU  
>gi|94923|pir||S15169

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)  
 pseudobactin uptake protein [*Pseudomonas putida*]Length = 819  
 Score = 152 bits (381), Expect = 6e-36  
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTHSLTAGTRFNVVTGRLHLLGGLHYTRYETSQTKDM 494  
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y  
 Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDLHLLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPTYAGITYDLTPQQSIYGSYTKIFKQQ 554  
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q  
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRLNASFALFYLEQKNRTVVDFGYVPGAGGK 614  
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG  
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMVKRDNLAESTNEVVPDSGGL 668

Query: 615 QGSFQTVAKPIGKVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674  
 S + + +G + ELSGE+ W VF GY++ ++  
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFREGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727  
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +  
 Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWKLTLLGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783  
 RY + + +L N+ + Y Y G+ YG PR ++ L + F  
 Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq

1	ATGAATCAAA	ATCATTTTTC	ACTTAAAATT	CTGACCGTTA	TGCTGTTATC
51	GGCTTACGGT	GGTTCTTTTG	CAGACGGTGT	TGTGCCTGTT	TCAGACGGCA
101	ATACCGTCAG	TCTGGATACG	GTCAATGTAC	GCGGCTCTCA	TGCTTTGTTG
151	GGCAAGACCG	AAAAGACCCG	TTCTTATACG	ATAGATCGGA	TGTCCACCGC
201	CACAGGTATG	AGGATTGCGG	GCAAGGATAC	GCCGCAGTCG	GTCAGCGTCA
251	TCACGCGCAG	CCGCCTTGAC	GATAAGGCGG	TGCATACGCT	TGAAGAGGCA
301	ATGAAAAACA	CGACGGGTGT	CAACGTTGTG	CGCGATTTCAG	GCTTGCAGAC
351	GCGGTTTTTG	TCACGCGGTT	TCTATATTGA	TCAGATTGGT	GAAGACGGTA
401	TGACCGTCAA	TGTTGCAGGC	CGTTCGGGAT	ATACGGCGAA	AATCGACGTG
451	TCTCCGAGTA	CCGATTGGGC	GGTTTATGAC	CATATTGAAG	TTGTACGGGG
501	TGCAACGGGG	TTGACCAAT	CCAATTCAGA	GCCGGGAGGA	ACCGTCAATT
551	TGATCCGTAA	GTGA			

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep

1	MNQNHFSLKI	LTVMLLSAYG	GSFADGVVPV	SDGNTVSLDT	VNVRGSHALL
51	GKTEKTRSYT	IDRMSTATGM	RIAGKDT PQS	VSVITRSRLD	DKAVHTLEEA
101	MKNTTG VNVV	RDSGLQTRFL	SRGFYIDQIG	EDGMTVNVAG	RSGYTAKIDV
151	SPSTD LAVYD	HIEVVRGATG	LTQSNSEPGG	TVNLIRK*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq

1	ATGAATCAAA	ATCATTTTTC	ACTTAAAATT	CTGACCGTTA	TGCTGTTATC
51	GGCTTACGGT	GGTTCTTTTG	CAGACGGTGT	TGTGCCTGTT	TCAGACGGCA
101	ATACCGTCAG	TTTGGATACG	GTCAATGTAC	GCGGCTCTCA	TGCTCTGTCTG
151	GGCAAGACCG	AGAAGACCCG	TTCTTATACG	ATAGATCGGA	TGTCCACCGC
201	CACAGGTATG	AGGATTGCGG	GCAAGGATAC	GCCGCAGTCG	GTCAGCGTCA
251	TCACGCGCAG	CCGCCTTGAC	GATAAGGCGG	TGCATACGCT	TGAAGAGGCA
301	ATGAAAAACA	CGACGGGTGT	CAACGTTGTG	CGCGATTTCAG	GCTTGCAGAC

1212

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTTTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCAAT CCAATTGAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPOS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

	10	20	30	40	50	60
a743.pep	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT					
m743	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a743.pep	IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
m743	IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a743.pep	SRGFYIDQIGEDGITVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG					
m743	SRGFYIDQIGEDGMTVNVAGRSYGTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG					
	130	140	150	160	170	180
a743.pep	TVNLIRKR					
m743	TVNLIRKX					

g744.seq not found yet  
g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTTGGA TGAATTATGT GAACCAAATA TTTCTGTTTT AATCGGAGAA
151 AAGGGAAC TGAAAGACAGC ATATGCTGTT TATTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACGTGTTT AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGTATCC GGAATTTGTA
451 CAAGCAATAA CTTTAATAGA AAATCAAAA GAAGTCGCGG AAATGATTTT
501 TGGAAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTTG TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAAT ACCAACTTTC
851 AAGATAATTC AGTATTTTAA GACTGGAGGA CCGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGTAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
1001 GGAATGCTCC TAATTACAT GATGAGTATA AAAATTTAAC TTCATTATT
1051 AGCTTCCTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
1251 AAATTCCTCG AAATTTTTTG AATTTTAAA CGGGAAAGAT AGATTAAAT

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1213

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAT
1501 ATTTCTCCTA AAATAAAAC TGAAACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAGGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKTLEFG FVDAANYRRR ENKDLFNRIE VKGEYLDELG EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKEVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEEESQQ ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNQN TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQEQEKQD SLEKGSWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKKSKEYD VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLFY YSQSDYQNFEL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKEMS TANEFLQQLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTFFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AACTTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TGCGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTGT TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGTG GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFWQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAAAACAAA CGAAGTCCTG ACCGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGCGCA AACCGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAAATCCGC CGCCGAAAC GGGGAAACCG
251 CCGCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAAAACGTA GCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAAACCAAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

g746.pcp

1	MSENKQNEVL	TGYEQLKRRN	RRRLVTASSL	VAASCILLAA	ALSSDPADSN
51	PAPQAQGETA	TESQNTANTA	TPALKSAEN	GETAADKPQD	LAGEDKPSAA
101	DEISEPENVA	GAPLVILNDR	LEDSNIAKLE	ESEKLQQAET	AKTEPKQAKQ
151	RAAEKVSATA	DSTDTVAVEK	PKRTAEPKPO	KAERTAEPK	KAKETKTAEK
201	VADKPPTAAE	KTKPDTAKSD	SAVKEAKKD	KAEGKKTAEK	DRSDGKKHET
251	AQKTDKADT	KTAEKEKSGK	AGKKAAIQAG	YAEKERRALG	QRMKMAAGID
301	STITEIMTDN	GKQYRVKSSN	YKNARDAERD	LNKLRVHSLA	GOVTNE*

**m746.seq**

1	ATGTCGCAAA	ACAAACAAAA	CGAAGTCCTG	AGCGGTTACG	AACAACTCAA
51	ACCGCGCAAC	CGCCGCGCGC	TCGTAACGGC	AAGTTGCCTG	GTTGCCGCGCT
101	CTCTGCATCCT	GCTGGCAGGT	CGCCTCAGTT	CCGGCCCTCG	CGAACAGACT
151	GCCGCGCAAA	CAAGCGCGCT	AGAAAACAAA	CGCGCAGGTG	CGGCACAAAC
201	CCCTTGCCTTT	AAATTCGCGC	CCGACAAAC	GCAGGACTTG	GCAGGCGAAG
251	ACAAGCCTTC	TGCCGCGCAC	AGCGAAATCA	CGCAGCCTGA	AAACGTAAAG
301	CGCGCGCTGG	TGCTGATTAA	CGAGCGCCTC	GAAGACAGA	ACATCAACGC
351	TTTGGAAGCA	TCCGAGAAAC	TGCAACAGGC	AGAAACCGCC	AAAACCGCAC
401	CGAAGCAGGC	AAAACACACG	GCTGCGCAAA	AAGTGCCTGC	ACTGCGGCAC
451	AGTAGCGGATA	CGGTAGCGGT	TGAAAAAACG	AAACGCCACTG	CGCAAAACAA
501	ACCGCAAAAA	GCGGAACGCA	CTGCCAAAGC	CAAGCCCCAA	GCCAAAGAAA
551	CCAAAACCGC	CGAAAAGATT	GCCGCAAAAC	CGAAAACATG	CGCCGAAAAA
601	ACCAAACCGC	ATACCGGCAA	ATCCGACAGC	CGGTAAGAG	AAGCGAAAAA
651	AGCCGACAAG	GCTGAAAGCA	AAAAAACAGC	CGAAAAAGAC	TGCTCGGACG
701	GCAAAAACGA	CGAAACGGCA	CAAAAAACCG	ACAAGCGGGA	CAAGACGAAA
751	ACCGCCGAGA	AGGAAAAATC	CGGTAAGAAA	GCCGCCATT	AGGCAGGTTA
801	TGCCGAAAAA	GAACGCGCCT	TAAGCTTCCA	CGCAAAATG	AAGGCGCGG
851	GTATCGATT	GACCATACC	GAAATTATGA	CCGACAACGG	CAAAGTTTAC
901	CGCGTCAATT	GACCAACTA	TAAAAACGCA	AGGGATGCGG	ACAAGCGATT
951	GAACAAATTG	CGGTACACG	GTATCGCGG	TCAGGTAACG	AATGAATAG

m746.pcp

1	MSENKQNEVL	SGYEQLKRRN	RRRLVTASCL	VAASCILLAA	ALSSGPAEQT
51	AGETSGVENK	AAGAAQTPAL	KSAADKPQDL	AGEDKPSAAD	SEISEPENVG
101	APLVLINERL	EDSNSIKGLEA	SEKLQQAETA	KTAPKQAKOR	AAEKVPTAAD
151	STDTVAVEKP	KRTAETKPKQ	AERTAKAKPK	AKETKTAEKV	ADPKPTAAEK
201	TKPDTAKSDK	AVKEAKKADK	AESKKTAEKM	RSDGKKHETA	QKTDKADKTK
251	TAEEKSGSKK	AAIQAGYAEK	ERALSQRKMD	KAAGIDSTIT	EIMTDNGKVY
301	RVKSSNYKNA	RDAERDLNKL	RVHGIAGOVT	NE*	

### Homology with a predicted ORF from *N. gonorrhoeae*

**m746/g746** 89.9% identity in 346 aa overlap

```

      10      20      30      40      50
m746.pep  MSENKQNEVLVSGYEQLKRRNRRLVTASCLVAASCIILAAALSSGPAEQT----AGETSG
          |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746      MSENKQNEVLVTGYEQLKRRNRRLVTASSLVAASCIILAAALSSDPADSNPAPQAGETGA
          10      20      30      40      50      60

      60      70      80      90      100      109
m746.pep  VENKAAGAAQTPLKSA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
          :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746      TESQTANTAQTPLKSAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
          70      80      90      100      110      120

```

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	110	120	130	140	150	160	169
m746.pep	LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ						
	:     :     :     :     :     :     :						
g746	LEDSNIKGLEASEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPQ						
	130	140	150	160	170	180	
	170	180	190	200	210	220	229
m746.pep	KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK						
	:     :     :     :     :     :     :						
g746	KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK						
	190	200	210	220	230	240	
	230	240	250	260	270	280	
m746.pep	DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALSQRKMKAAAGID						
	:     :     :     :     :     :     :						
g746	DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALSQRKMKAAAGID						
	250	260	270	280	290	300	
	290	300	310	320	330		
m746.pep	STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX						
	:     :     :     :     :     :						
g746	STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX						
	310	320	330	340			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```
a746.seq
1  ATGTCCGAAA  ACAAACAAAA  CGAAGTCCTG  AGCGGTTACG  AACAACTCAA
51  ACGGCGCAAC  CGCCGCCGCC  TCGTAACGGC  AAGTTGCCTG  GTTGCCGCCT
101 CCTGCATCCT  GCTGGCAGCC  GCCCTCAGTT  CCGGCCCTGC  CGAACAGACT
151 GCGGCGGAAA  CAAGCGGCGT  AGAAAACAAA  GCGGCAGGTG  CGGCACAAAC
201 CCCTGCCTTG  AAATCCGCCG  CCGACAAACC  GCAGGACTTG  GCAGGCGAAG
251 ACAAGCCTTC  TGCCGCCGAC  AGCGAAATCA  GCGAGCCTGA  AAACGTAGGC
301 GCGCCGCTGG  TGCTGATTAA  CGACCGCCTC  GAAGACAGCA  ACATCAAAGG
351 TTTGGAAGCA  TCCGAGAAAC  TGCAACAGGC  AGAAACCGCC  AAAACCGCAC
401 CGAAGCAGGC  AAAACAACGC  GCTGCCGAAA  AAGTGCCGGC  AACTGCCGAC
451 AGTACGGATA  CGGTAGCGGT  TGAAAAACCG  AAACGCACTG  CCGAAACAAA
501 ACCGCAAAAA  GCGGAACGCA  CTGCCAAAGC  CAAGCCCAAA  GCCAAAGAAA
551 CCAAAACCGC  CGAAAAAGTT  GCCGACAAAC  CGAAAACTGC  CGCCGAAAAA
601 ACCAAACCGG  ATACGGCAAA  ATCCGACAGC  GCGGTAAGAG  AAGCGAAAAA
651 AGCCGACAAG  GCTGAAAGCA  AAAAAACAGC  CGAAAAAGAC  CGTTCGGACG
701 GCAAAAAACA  CGAAACGGCA  CAAAAACCG  ACAAAGCGGA  CAAGACCAAA
751 ACCGCCGAGA  AGGAAAAATC  CGGTAAAAAA  GCCGCCATTC  AGGCAGGTTA
801 TGCCGAAAAA  GAACGCGCCT  TAAGCCTCCA  GCGCAAAATG  AAGGCGGCGG
851 GTATCGATTG  GACCATCACC  GAAATTATGA  CCGACAACGG  CAAAGTTTAC
901 CGCGTCAAAT  CAAGCAACTA  TAAAAACGCA  AGGGATGCCG  AACGCGATTT
951 GAACAAATTG  CGGTACACG  GTATCGCCGG  TCAGGTAACG  AATGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```
a746.pep
1  MSENKQNEVL  SGYEQLKRRN  RRLVTASCL  VAASCILLAA  ALSSGPAEQT
51  AGETSGVENK  AAGAAQTPAL  KSAADKPQDL  AGEDKPSAAD  SEISEPENVG
101 APLVLINDRL  EDSNIKGLEA  SEKLQQAETA  KTAEPKQAKQ  RAEKVPATAD
151 STDTVAVEKP  KRTAETKPQK  AERTAKAKPK  AKETKTAEKV  ADKPKTAAEK
201 TKPDTAKSDS  AVKEAKKADK  AESKKTAEKD  RSDGKKHETA  QKTDKADKTK
251 TAEKEKSGKK  AAIQAGYAEK  ERALSQRKM  KAAGIDSTIT  EIMTDNGKVY
301 RVKSSNYKNA  RDAERDLNKL  RVHGIAGQVT  NE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

	10	20	30	40	50	60
a746.pep	MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK					
	:     :     :     :     :     :					
m746	MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK					
	10	20	30	40	50	60

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```

          70      80      90      100      110      120
a746.pep  AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
          |||||
m746      AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA
          70      80      90      100      110      120

          130      140      150      160      170      180
a746.pep  SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQKAERTAKAKPK
          |||||
m746      SEKLOQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQKAERTAKAKPK
          130      140      150      160      170      180

          190      200      210      220      230      240
a746.pep  AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          |||||
m746      AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          190      200      210      220      230      240

          250      260      270      280      290      300
a746.pep  OKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY
          |||||
m746      OKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY
          250      260      270      280      290      300

          310      320      330
a746.pep  RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||||
m746      RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          310      320      330

```

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2558; ORF 747&gt;:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPPYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2560; ORF 747.a&gt;:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPPYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

**a747/m747** 97.1% identity in 102 aa overlap

	10	20	30	40	50	60
a747.pep	LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR					
m747	LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR					
	10	20	30	40	50	60

  

	70	80	90	100
a747.pep	HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSXX			
m747	HKTIYKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSXX			
	70	80	90	100

**a747/m80195**

gi|150271 (M80195) outer membrane protein [Neisseria meningitidis] Length = 272  
 Score = 59.3 bits (141), Expect = 6e-09  
 Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGSVIGLNVGKQLTDSVGLFDPYYR 60  
 + PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+  
 Sbjct: 174 INPWSEVKFDLNSRYKLNTGVTNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95  
 +T + E + GD + ++ EYG RV F  
 Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

**g748.seq**

```

1 ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51 CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTAT TTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACGCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCGCGG
201 GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAAG CCTTCAACCC CGACGGATTG ACCGTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCCGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TCGGACGGCG ATTTGAGCCT GCAAATCTGC GCCTTCACCC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAAACA CACCGCCCAA
601 ACCGCGGTCA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCGAGAC GGCACGGGCA
701 ACCCAAGGT TTCCGATCCC AAAACCGCCG ACGAGGTTT ATGGACGGGC
751 GTGGCGGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGAAAATA CAGCGGGGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTCG CCAAAGACCC
951 CGAGGTGAT ATCAGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCAAA AACACTGCC TCTTCGCGG CGCCTACAGC
1051 TATTCTCGCG GACCGCCTC AAGCGGACAG CTGTATGTCG GGCTGGTGTT
1101 CGCTGCTAT CAGGCAAATC TTGCCGACGG TTTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTCG TCTTGCCCGG CGTGGGAAA GCGGATCTT TGGGACAAGG
1251 GCTGCCGGGC GTATAA
  
```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

**g748.pep**

```

1 MSONQPAQPT KRNLFKTLA VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPROAF SIMCAFDVTA QSAKQLENLF RTLTAIEFL
101 TQGGEYQDGD DKLPASAGSI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KTVHLQEMRD FPNDKLOKSW CDGDLQLQIC AFTPETCQTA LRDIIKHTAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLOEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLLNGEPL EEYISPFGGG
  
```

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401 YFFVLPGVGK GGFLGQGLPG V\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq

```

1 ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51 CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAAACAGG CGAAACCGCC GAACGCACCG CCGAAAGCCA AACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTTG ACCGTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATTG ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAAGCTTG TGCAGCGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCAGGGAC GGCACGGGCA
701 ACCCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTTT GTGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTGGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGCAAATA CAGCGGTGCG
901 CGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGGCCCA AAGACAGCCA TATACGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCAAAA AAACACCGCC TCTTCGCGCG CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGCTGTT
1101 CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGCCCGG CGTGGAAAAA GGCGGCTTTT TGGGGCAAGG
1251 GCTGCTGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep

```

1 MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGGYQDGD DKLPPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNKDLQKSW CDGDLQLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEQT D IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNNGEPL EEYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

```

m748.pep      10      20      30      40      50      60
MSKKQPAQPT RRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPQAYPCYGEHQ
g748          10      20      30      40      50      60
MSQNQPAQPTKRNLFKTALAVGAIGAIGGYFGGKKQGETAERTAESQHSPQAYPCYGEHQ

m748.pep      70      80      90      100     110     120
AGIVTPQQA F SIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGYQDGD DKLPPAGSGI
g748          70      80      90      100     110     120
AGIVTPRQA F SIMCAFDVTAQSAKQLENLFRILTARIEFLTQGGYQDGD DKLPSAGSGI

m748.pep      130     140     150     160     170     180
LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNKDLQKSWCDGDLQLQIC
g748          130     140     150     160     170     180
LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKTVHLQEMRDFPNKDLQKSWCDGDLQLQIC

m748.pep      190     200     210     220     230     240
AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP

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**a748.seq**

1	ATGAGCAAAA	ACCAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAC
51	CGCGATCGCA	GCTGGAGCAG	TCGGCGCAAT	CGGAGGTTAT	CTCGGGCGCA
101	AAAAACGGGG	CGAAACCGCC	GAACGCAACC	CCGAAAGCCA	CTACTCGCCC
151	CAAGCCTATC	CTGTCTACGG	CGAACATCAG	CGAGGCATCG	TATCGCGCA
201	GCAGGCTGTT	TCGATTATGT	GCGCCTTCGA	CGTAACCCGG	CBAAGTGCCA
251	AGCAGCTGTA	AAACCTGTTC	CGCAGCGCTA	CCGCCCGCAT	CGAGTTTCTC
301	ACCAAGGGCG	CGGAATACCA	AGACGGCGAC	CGCAAACTTC	CGCCAGCCGG
351	CAGCGGCATT	TTGGGCAAG	CCTTCAACCC	CGACGGGTGT	ACCGTTACCG
401	TGGGGGTTGG	CATTGACCTG	TTTGACGGCC	GGTTCGGACT	CAAGAACAAA
451	AAACCGATTC	ATTTCGAGGA	AATGCGCGAC	TTTCTCAAAG	ATAAGCTGCA
501	AAAAAGCTGG	TGCGACGGCG	ATTTGAGCCT	GCAAATCTGT	GCCTTACCCC
551	CCGAAACCTG	CCAAGCCGCC	CTGCGCGACA	TCATCAAAAC	CACCGTCCAA
601	ACCGCCGTTA	TCGCGTTGAG	TATCGACGGG	TGGCAGCCTA	AATCCGAACC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCCGCGAC	GGCACGGGCA
701	ACCCCAAAGT	TTCCGACCCC	AAAACCTCCG	ACGAGGTTTT	GTGGACGGGG
751	GTGGCCGCCA	ACAGCCTCCA	CGAACCGGAG	TGGGCGAAAA	ACGGCAGTGA
801	TCAGGCAGTC	CGCCTTATCC	GCCACTTTGT	TGAGTTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAAACGAC	ATTTTCGGCG	GGCGCAAAAT	CACGCGCCGC
901	CGATGTGACG	GCAAAAAGAG	AGCCGACCAA	CCGGATTTTG	CCAAAGATCC
951	CAGGGGGAAT	ACCACGCCCA	AAGACAGCCA	TATACGCCTG	GCGAATCCGC
1001	CGCATCCCGA	GTTCTTTAAA	AAACACCGCC	TCTTCCGCCG	CGCCTACACG
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTCG	GGCTGGTGTT
1101	CGTCTGCTAT	CAGGCAAAAC	TGCGCGACGG	ATTACTTCTC	GTGCAAAACG
1151	TCCTCAACGG	CGAAGCCGTG	GAAGAATACA	TCAGCCCTTT	CGGCGGCGGC
1201	TATTTCTTCG	TCTTGCCCGG	CGTGAAAAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGGC	GATATAA			

a748.ppt

1	MSKNQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKRGETA	ERTAESQHSP
51	QAYPCYGEHG	AGIVTPQQAF	SIMACFDVTA	QSAQKLENLF	FLTRATIEFL
101	TGGEGYQDGD	DKLPFAGSGJ	LGKAFNPDGL	TVTGVGSSLF	RDTGRFLGKL
151	KPIHLQEMRD	FSNDKLQKSW	CDGDLSLQIC	AFTPETCQAA	LRDIIKHTVQ
201	TAIVIRWISD	WQPKSEPGAM	AARNLLSGRD	GTGNPKVSDP	KTAEVLVWGS
251	VAANSLEDEP	WAKNGSYQAV	RLRIHFVEFD	DRTPLQEQTD	IFGRKKYSGA
301	PMDGKKEADQ	PDFAKDPEGN	TPPKDSHIRL	ANPRDPEFLK	KHRLFRRAYS
351	YSRGLASSGG	LDVGLVVFVCY	<u>QANLADGFIF</u>	<u>VQNLLNGEPL</u>	EYIISPFGGG
401	YFFVLPGEVK	GGFLGQGLLG	V*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

a748.pep	MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSPQAYPCYGEHQ
m748	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPQAYPCYGEHQ
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRITLTARIEFLTQGGEYQDGDGDKLPPAGSGI
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRITLTARIEFLTQGGEYQDGDGDKLPPAGSGI
a748.pep	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSLQIC
m748	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSLQIC
a748.pep	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
m748	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
a748.pep	KTADDEVLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQTDIFGRRKYSGA
m748	KTADDEVLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQTDIFGRRKYSGA
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ
m748	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ
a748.pep	LDVGLVFVCYQANLADGFIQVQNLNNGEPLLEEYISPFGGGYFFVLPVGEKGGFLGQGLLG
m748	LDVGLVFVCYQANLADGFIQVQNLNNGEPLLEEYISPFGGGYFFVLPVGEKGGFLGQGLLG
a748.pep	VX
m748	VX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATGTGCC	GTGATGCTTG	CCTTGGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCCGCGCCG	GCCGCGTCCG
101	GTGAGACCCA	ATCCGCCAAC	GAAGCGGTT	CGGTCGGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCGAT	GAATCTGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AGGGCGTGAT	GGTGGTGGAC	GAACGCGAAA	ATATCGCCCC	GGGGCTTTCC
301	GACAAAATGA	CCGTAAccct	GCTGCCGGGC	GAATACGAAA	TGACCTGCGG
351	CCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAGCCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGCCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTACGTTCA	AGGCGAGGTT	AAAGAGCTGG	CGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGCCACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGTGTG	AAGACGACTT
651	CAAAGACGGT	GCGAAAGATG	CCGGGTTTAC	CGGCTTCCAC	CGTATCGAAC
701	ACGCCCTTTG	GGTGGAAAAA	GACGTATCCG	GCGTGAAGGA	AACCGCGGCC
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC



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801 GttccctCCG GGCAAAGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TGCGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCTGTCG TTGATTGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCATA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

g749.pep

```

1 MRKFNLTAALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQVN
51 DNACEPMNLT VPSGQVVFNI KNSGRKLEW EILKGVMVVD ERENIAPLGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPIV DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDNTFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

```

1 ATGAGAAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCACTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAACGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAACTTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAACATGATG CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTTGG
801 GTTCTCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
951 GTTCCGTCCG CTGATCGAGG CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCTT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

m749.pep

```

1 MRKFNLTAALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQVN
51 DNACEPMELT VPSGQVVFNI KNSGRKLEW EILKGVMVVD ERENIAPLGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDNTFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

m749.pep      10      20      30      40      50      60
MRKFNLTAALSVMALALGLTACQPPEAEKAAPASGEAQTANEGGSVSIQVNDNACEPMELT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g749          10      20      30      40      50      60
MRKFNLTAALSVMALALGLTACQPPEAEKAAPASGETQSANEGGSVGIQVNDNACEPMNLT

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	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELFSELD PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRVHYERIEPIAELFSELD PVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVG GASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVG GASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDG FETYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDG FETYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

1	ATGAGAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGGCGGTT	CGGTCAGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCAGT	GGAACAGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAATGA	CCGTCACCCT	GTGCGCGGC	GAATACGAAA	TGACTTGGCG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCTG	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCTCTCC	GGCAAGGTGG	TCGGCGGCGC	GTCCGAATG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCCGTCCG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTTG	GAAAAAACCG
1001	ATACCAACTT	CAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAA			

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

1	MRKFNLTALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSIHAVN
51	DNACEPMELT	VPSGQVVFNI	KNNSGRKLEW	EILKGMVVVD	ERENIAPGLS
101	DKMTVTLLPG	EYEMTCGLLT	NPRGKLVVTD	SGFKDTANEA	DLEKLSQPLA
151	DYKAYVQGEV	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPVI	DAREDDFKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKEIAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVG GASEL	IEEVAGSKIS	GEEDRYSHTD

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301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK  
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

**a749/m749** 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNL	TALSVMLALGLTACQP	PEAEKAAPASGEAQTANEGGSV	SI	AVNDNACEPMELT	
m749	MRKFNL	TALSVMLALGLTACQP	PEAEKAAPASGEAQTANEGGSV	SI	AVNDNACEPMELT	
	10	20	30	40	50	60
a749.pep	70	80	90	100	110	120
a749.pep	VPSGQV	VFNKNN	SGRKLEWEILKGV	MVVD	DERENIAPGLSDKMTVTLLPGEYEMTCGLLT	
m749	VPSGQV	VFNKNN	SGRKLEWEILKGV	MVVD	DERENIAPGLSDKMTVTLLPGEYEMTCGLLT	
	70	80	90	100	110	120
a749.pep	130	140	150	160	170	180
a749.pep	NPRGKLV	VTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE				
m749	NPRGKLV	VTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE				
	130	140	150	160	170	180
a749.pep	190	200	210	220	230	240
a749.pep	KAKSLFADTRVHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
m749	KAKSLFADTRVHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
	190	200	210	220	230	240
a749.pep	250	260	270	280	290	300
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKV	VVGASELIEEVAGSKISGEEDRYSHTD				
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKV	VVGASELIEEVAGSKISGEEDRYSHTD				
	250	260	270	280	290	300
a749.pep	310	320	330	340	350	360
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTD	TNFKQVNEILAKYRTK	DGFETYDKLG			
m749	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTD	TNFKQVNEILAKYRTK	DGFETYDKLG			
	310	320	330	340	350	360
a749.pep	370	380	389			
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

**g750.seq**

1	GTGAAACCGC	GTTTTATTG	GGCAGcctGC	GCCGTCCTGC	CGGCCGCCTG
51	TTCGCCCGAA	CCTGCCGCCG	AAAAAACTGT	ATccgCCGCA	TCCCAAGCCG
101	CATCCACACC	TGTCGCCACG	CTGACCGTGC	CGACCGCGCG	GGGCGATGCC
151	GTTGTGCCGA	AGAATCCCGA	ACgcgctgcc	gtgtAcgaCt	ggCGGCGTt
201	ggaTACGCTG	ACCGAGCCGG	GCGTGAATGT	GGGCGCAACC	ACCGCGCCGG
251	TGCGCGTGGA	CTATTGCGAG	CCTGCATTG	ACAAGCGCGG	AACGGTGGGG
301	ACGCTGTTTG	AGCCCCGATTG	CGAATCCCTG	CACCGCCACA	ATCCCGAGTT
351	TGTCATTACC	GGCGGGCCGG	GTGCGGAAGC	GTATGAACAG	TTGGCGAAAA
401	ACGCGACCAC	CATAGATTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC
451	GGCGAGAAGC	AGATGGAGAC	CCTGTCGCGG	ATTTTCGGTA	AGGAAGCGCG
501	CGTGGCGGAA	TGGAATGCGC	AGATTGACGC	GCTGTTCGCC	CAAAAGCGCG
551	AAGCCGCCAA	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCGGT	TACAGGCAAC
601	AAGGTGTCCG	CCTTCGGCAC	GCAATCGCGG	TTGGCAAGTT	GGATACACGG
651	CGACATCGGC	CTGCCGCCCG	TGGACGAATC	TTTACGCAAC	GAAGGGCACG
701	GGCAGCCCGT	TTCTTCGAA	TACATCAAAG	AGAAAACCC	CGGCTGGATT
751	TTTCATCATCG	ACCGCACCGC	CGCCATCGGG	CAGGAAGGGC	CGGCTGCCGT

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801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAGCGCA  
 851 AGCAAATCAT CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCGCG  
 901 CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC  
 951 AGAACCCGTT GCGGCGCAGT AG

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

g750.pep  
 1 VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA  
 51 VVEKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLO PAFDKAATVG  
 101 TLFEPPCESL HRHNPQFVIT GPGAEAYEQ LAKNATTIDL TVDNGNIRTS  
 151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKGKG RGLVLSVTGN  
 201 KVSAFGTQSR LASWIHGDIG LPPVDESLRN EGHGQPVSEF YIKEKNPGWI  
 251 FIDRTAAIG QEGPAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA  
 301 RQLIQAAEQL KAAFEKAEPV AAQ\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

m750.seq  
 1 GTGAAACCGC GTTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG  
 51 TTCGCCCGAA CCTGCCGCGC AAAAAACTGT ATCCGCCGCA TCCGCATCTG  
 101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG  
 151 AATCCCCGAA GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC  
 201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT  
 251 ATTTGCAGCC TGCATTGAC AAGCGGCGAA CGGTGGGGAC GCTGTTTCGAG  
 301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG  
 351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA  
 401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG  
 451 ATGGAGACCT TGGCGCGGAT TTTCCGGCAAG GAAGCGCGCG CGGCGGAATT  
 501 GAAGGCGCAG ATTGACGCGC GTTTCGCCCA AACGCGCGAA GCCGCCAAAG  
 551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCCGCC  
 601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT  
 651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT  
 701 CCTTCGAATA CATCAAAGAG AAAAACCCTG ATTGGATTTT CATCATCGAC  
 751 CGTACCGCCC CCATCGGGCA GGAAGGGCCG GCGGCTGTCG AAGTATTGGA  
 801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG  
 851 TCATGCGCTG CGCGAACTAC ATTGTCGCGG GCGGCGCGCG GCAGTTGATT  
 901 CAGGCGGCGG AGCAGTTGAA GCGGCGGTTT AAAAAGGCAG AACCCGTTGC  
 951 GCGGGGGAAG AAGTAG

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

m750.pep  
 1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK  
 51 NPERVAVIDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE  
 101 PDYEALHRYN POLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ  
 151 METLARIFGK EARAELKAO IDALFAQTRE AAKGKGRGLV LSVTGNKVSA  
 201 FGTQSRLASW IHGDIGLPPV DESLRNEGHG QPVSEFYIKE KNPDWIFIID  
 251 RTAAIGQEGP AAVEVDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI  
 301 QAAEQLKAAF KKAEPVAAGK K\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

	10	20	30	40	50
m750.pep	VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASA-----ATLTVP TARGDAVVPKNPERVA				
	:       :       :       :				
g750	VKPRFYWAACAVLPAACSPEPAAEKTVSAAASQAASTPVATLTVP TARGDAVVPKNPERVA				
	10	20	30	40	50
	60	70	80	90	100
m750.pep	VYDWAALDTLTELGVNVGATTAPVRVDYLOPAFDKAATVGTTLFEPPDYALHRYNPQLVIT				
	:       :       :       :				
g750	VYDWAALDTLTEPGNVNVGATTAPVRVDYLOPAFDKAATVGTTLFEPPDCESLHRHNPQFVIT				
	70	80	90	100	110
	120	130	140	150	160
m750.pep	GGPGAAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFA				
	:       :       :       :				

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```

g750      GGFGAEAYEQLAKNATTIDLTVDNGNI RTSGEKQMETLSRIFGKEARVAELNAQIDALFA
           130      140      150      160      170      180

           180      190      200      210      220      230
m750.pep  QTREAAKGKGRGLVLSVTGNKVS AFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF
           |||||||||||||||||||||||||||||||||||||||||||||||||||
g750      QKREAAKGKGRGLVLSVTGNKVS AFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF
           190      200      210      220      230      240

           240      250      260      270      280      290
m750.pep  YIKEKNPDWIFIIDRTAAIGQEGPAAVEVDNALVRGTNAWKRKQIIVMPAANYIVAGGA
           |||||||||||||||||||||||||||||||||||||||||||||||||||
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVDNALVCGTNAWKRKQIIVMPAANYIVAGGA
           250      260      270      280      290      300

           300      310      320
m750.pep  RQLIQAAEQLKA AFKAEPVAAGKKX
           |||||||||||||||
g750      RQLIQAAEQLKA AFKAEPVAAQX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1   GTGAAACCGC  GTTTTATTG  GGCAGCCTGC  GCCGTCCTGC  TGACCGCCTG
51  TTCGCCGAA  CCTGCCGCCG  AAAAACTGT  ATCCGCCGCA  TCCGCATCTG
101 CCGCCACACT  GACCGTGCCG  ACCGCGCGGG  GCGATGCCGT  TGTGCCGAAG
151 AATCCCGAAC  GCGTCGCCGT  GTACGACTGG  GCGGCGTTGG  ATACGCTGAC
201 CGAATTGGGT  GTGAATGTGG  GCGCAACCAC  CGCGCCGGTG  CGCGTGGATT
251 ATTTGCAGCC  TGCATTGAC  AAGGCGGCAA  CGGTGGGGAC  GCTGTTTCGAG
301 CCCGATTACG  AAGCCCTGCA  CCGCTACAAT  CCTCAGCTTG  TCATTACCGG
351 CGGGCCGGGC  GCGGAAGCGT  ATGAACAGTT  GGCGAAAAAC  GCGACCACCA
401 TAGATCTGAC  GGTGGACAAC  GGCAATATCC  GCACCAGCGG  CGAAAAGCAG
451 ATGGAGACCT  TGGCGCGGAT  TTTCGGCAAG  GAAGCGCGCG  CGGCGGAATT
501 GAAGGCGCAG  ATTGACGCGC  TGTTCGCCCA  AACGCGCGAA  GCCGCCAAAG
551 GCAAAGGACG  CGGGCTGGTG  CTGTCGGTTA  CGGGCAACAA  GGTGTCCGCC
601 TTCGGCACGC  AGTCGCGGTT  GGCAAGTTGG  ATACACGGCG  ACATCGGCCT
651 ACCGCCTGTA  GACGAATCTT  TACGCAACGA  GGGGCACGGG  CAGCCTGTTT
701 CCTTCGAATA  CATCAAAGAG  AAAAACCCCG  ATTGGATTTC  CATCATCGAC
751 CGTACCGCCG  CCATCGGGCA  GGAAGGGCCG  GCGGCTGTCG  AAGTATTGGA
801 TAACGCGCTG  GTACGCGGCA  CGAACGCTTG  GAAGCGCAAG  CAAATCATCG
851 TCATGCCTGC  CGCGAACTAC  ATTGTGCGGG  GCGGCTCGCG  GCAGTTGATT
901 CAGGCGGCGG  AGCAGTTGAA  GGAGGCGTTT  GAAAAGGCAG  AACCCGTTGC
951 GGCGGGGAAA  GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1   VKPRFYWAAC  AVLLTACSPE  PAAEKTVSAA  SASAATLTVP  TARGDAVVPK
51  NPERVAVYDW  AALDTLTELG  VNVGATTAPV  RVDYLQPAFD  KAATVGTLFE
101 PDYEALHRYN  POLVITGGPG  AEAYEQLAKN  ATTIDLTVDN  GNIRTSGEKQ
151 METLARIFGK  EARAELKAQ  IDALFAQTRE  AAKGKGRGLV  LSVTGNKVSA
201 FGTQSRLASW  IHGDIGLPPV  DESLRNEGHG  QPVSFYEIKE  KNPDWIFIID
251 RTAAIGQEGP  AAVEVDNAL  VRGTNAWKRK  QIIVMPAANY  IVAGGSRQLI
301 QAAEQLKEAF  EKAEPVAAGK  E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

```

a750/m750  98.8% identity in 321 aa overlap

           10      20      30      40      50      60
a750.pep  VKPRFYWAACAVLLTACSPEPAAEKTVSASASAAATLTVP TARGDAVVPKNPERVAVYDW
           |||||||||||||||||||||||||||||||||||||||||||||||||||
m750      VKPRFYWAACAVLLTACSPEPAAEKTVSASASAAATLTVP TARGDAVVPKNPERVAVYDW
           10      20      30      40      50      60

           70      80      90      100     110     120
a750.pep  AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG
           |||||||||||||||||||||||||||||||||||||||||||||||||||
m750      AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEYIKE					
m750	AAKGKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFYEYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVLNVLNRGTNAWKRRQIIVMPAANYIVAGGSRQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVLNVLNRGTNAWKRRQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAFKAEPVAAAGKEX					
m750	QAAEQLKAAFKKAEPVAAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```

1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CCGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTTGGTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTCTCTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTCAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CGGAGGTGCC AAAAGCAGGT ACAAAGAAT TTGATGACTA TGTAAAAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAATCTAA
951 ACCCATACTG GTAGAACCAA ACAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2580; ORF 751&gt;:

m751.pep..

```

1  MAWSMFATTQ ADRAVRSATA PKEMWFHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAKQNR NSTNGSGVIA
101 VMNPPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVQKMNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFIGNKWIPF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKEFDDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKTCDNE KYEKEAF*

```

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

```
m752.seq.
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAAGATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAATAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGACAG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGCGG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTT CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAACACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCTT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```
m752.pep
1  MKISRPPEFT LLQQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHFFGD
301 GNGRTARALF YWFMLNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTIFYIYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPPK
451 SGNALAYVAP QDLLERLEKK *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

```
m752-1.seq
1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAATCAAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAAGATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
```

```

651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTT CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTT TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCCT ATTTCACTTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTGT GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQWFVFCPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEAITSAQLE GAATTRKVKAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFII PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTFFIYYQC DIKRAVADL EHYISDKQKH QOEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIETAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTTCTTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAI WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLED RHLRDNSDWN
101 CGDNIWLIQW FAPLGSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet



g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTGT GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CTTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTCTTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCCTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MMKSILTVSG NMRKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVROND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANFLC MQTIKQAGIA VAQTSLESDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDL SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKPTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAAACCA
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAATGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGTA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

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This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep.
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
 51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLESIDL AQFIADGVYQ
101 AKQAFLLQRVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCA AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QDMPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCA AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QDMPKIRSA TLVALTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYAE LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLRYRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVVPYGAELVSDGNFTAV					
a756	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVVPYGAELVSDGNFTAV					
	130	140	150	160	170	180
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGCGC ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCAC TGACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2596; ORF 757&gt;:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTKADK
101 ITAVRVVWNT DAMPQKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGGAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGCGCGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA

```

1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAACCT GGTGGAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151  GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GTTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

m758.pep	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
	10	20	30	40	50	60
m758.pep	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPA GSVGIGGSQT					
	70	80	90	100	110	120
m758.pep	130	140	150	160		
	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTCCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCACCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTTCTCAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAG
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGGACT
401  ACGACTACCA CCTTCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

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451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA  
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG  
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG  
 601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA  
 651 AAACCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA  
 701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTTCGACAAG  
 751 CATGAAAACC GCTGGGTGCT TGCGGGCGTA CTCAGCACCT ACGCCGGCTT  
 801 CGATAATTTC TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT  
 851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC  
 901 GAACTCATAT GGC CGCAGCAA CGGTAATGGC AACAGCACCC TGCAAGGGCT  
 951 CAACGAACGC ATCACCTGTC CCATTGCAAA CCCTTCGCTT GCCCCACAAA  
 1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA  
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA  
 1101 AGGCGCAGGC GCATTGCAGT TCGACAGCAA CTTACCGTTC GTCGGTAAAA  
 1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC  
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC  
 1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA  
 1301 TCGGGGAAGG CACTGTCGTA CTCGCCAAA AAGCTGCTTC AGACGGCAGC  
 1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT  
 1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA  
 1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTTT TACCCATATC  
 1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC  
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCG  
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA  
 1651 TACATCAACC CGCACCGCAA CCGTCGGACC GACTACTTCA TACTCAAACC  
 1701 CGGCGGCAAC CCGCGCAAT TTTTCCCGTT AAATATGAAA AACTCAACAA  
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCCGA ACAAGTCGCC  
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG  
 1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG  
 1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC  
 1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA  
 2001 ACGCACCGAC AGCACGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG  
 2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC  
 2101 CATGCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG  
 2151 GACCAGCGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCCC  
 2201 GACTGACGGC AGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA  
 2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACGGGA  
 2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCCG  
 2351 TTTTAAAGAG CGAAAACTAT CGTGCACTAC CTGCAACGCA AGTACGCGGC  
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT  
 2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCATCCGC ATGGAACGAG  
 2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT  
 2551 GACGGCGCAC AAATTACCCT GAACCCCGAT TTCGCCAATA ATACACACAA  
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCCGGC  
 2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC  
 2701 AAAC TGGAAG GGGACAGCCG CGGCGCATTC CAAATCCACG TCAAAACACAC  
 2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCATTGTG AGCCTCAATC  
 2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT  
 2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAAA AACAACAACG GATACAGCCT  
 2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGCGG  
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC  
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC  
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT  
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTTCTGACG  
 3151 GTGCCCCAAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG  
 3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG  
 3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC  
 3301 AAAGCACGGC AAGGCGGCGA TGCGCAAGCC GTCGAAACAG CCCGGCACGC  
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAAATCCAC AGTTTGAAAA  
 3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAC GATCAGCCGG  
 3451 TCGGCCAACA CCGCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA  
 3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA  
 3551 ACATCTGGCT GGAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA  
 3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC  
 3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA  
 3701 CAAACAACCG TTTTGATGAA GGCGTATCCG CCCGAAACCG CAGCAACGGC

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

m759.pep

```

1 MRFTHTTFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGFTV
51 GASNISIQDK QGKILGRVLN GIMPEDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLL NGQPKANAYL DTDREPYFVR LSGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLEAFDK
251 HENRWVLAVG LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNSRHRMP SEDAGKTLIL
351 SSRFDNKTLM LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRDL NGNNLAFTHI
501 RHADGGAQIV NHPDQAATL TLGNPVLSP EHVEWVQWGN RPOGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLNGGMN LNGEVLEIEG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDTA
751 YDLSGIDLGF TQGKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDRSEL RLKKAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALT
851 DGAQITLNPD FANNTNNRF NTLTVNGTLD GFGTFRFLT IVRKQNAAPL
901 KLEGDSRGAF QIHVKNTGQE PQTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQ AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESLD
1101 KARQGGDAQ VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEILSR
1151 SANTAVSEQA AYNTGRQOAG RRIDRHLTDP QQQNIWLETG TQQT DYHSGT
1201 HRPYQOTTNY AHIGIQTGIT DRLSVGTILT DERTNNRFE GVSARNRSG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTHW AGIRLDKTV
1351 LGQAKLTAF SSDYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

g760.seq (partial)

```

1 AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

g760.pep (partial)

```

1 NNRNTRYAAL GKRVMGVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
51 DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1   ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCACG CTGCCAACCC TGTTCGCCTT CGACCGCGTG
451 GAAGTGATGC CGGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATTGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCGCG CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTAAAATGC ACAGCCACGA CGTGTTCCGC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGC CTTGCGCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTGTATGC CAAGACGGTG TTCCGTCTCT TGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCAG TTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCGT TACGCCGAT TGGGCAAAAC
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGAT ACATGACGGC
1951 GGTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAC
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTCCGA GCGCAGCCTG
2101 ACGGCAAACC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1   MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKQ QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFADFDRV
151 EVMRGPISGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THQYKAEAD
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQORR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSHDVFA
301 DLKHYFGNGG YGKVGMYSD RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKAFAYDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSVSLD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRETPKLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSFYRMKDKNAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
g760				NNRNTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30

  

	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGI FLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGI FLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90

  

	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGSESTFNIPGSESLTANL					
g760	AGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGSTNTFNIPGSESLTANL					
	100	110	120	130	140	150

  

	709
m760.pep	RYSEFX
g760	RYSEFX

  

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAATAT	CATTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTTCC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGCGC	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TGCCCATCCG	TCTCACCAGC	GAAGTCGGGC	GCGCCAATTTC
651	GTTCGCGAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTG
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCGA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTCGC	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTGTGA	AACCACTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCCGATTG	AAATTCGTCC
1301	TCCGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACTCACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTGAGCAT	CGATACGTTG
1501	TCTTCCGCGG	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGCGGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA



1237

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTAT ACCTCCGACG AAAACCTCTA CGGCGAAATC GCGGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACCTAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

m761.pep

```

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLT L
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

a761.seq

```

1 ATGAAATAT CATTTTATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCGG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGGAA AGCATTTTCC TGC GCGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGGCGGGTG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTTCGTG GGCAAACCGC AGCCTGAATA TGACATCAA CGAAGTGCTG
601 AACAACAAACG TCGCCATCCG TCTACCGGCG GAAGTCGGGC GCGCCAATTC
651 GTTCCGCGAG GGCATAGACA GCAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAACG CGACAACGCG TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG GTACGACCG
801 CTTCCGACTG CTTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCTT
1151 TTTCCGCCCT CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCGATTG AAATTCTGTC
1301 TCGGCGGCGG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCCGCGG TGTTCAACGC CGACCCGAG TACACCGGCC AATACGAAAC
1551 CCGCGTGAAG AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGCA TCCAAAAAAC
1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTTCG GCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1238

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTND NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

m761.pep	10	20	30	40	50	60
	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
m761.pep	70	80	90	100	110	120
	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
m761.pep	130	140	150	160	170	180
	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
	130	140	150	160	170	180
m761.pep	190	200	210	220	230	240
	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
	190	200	210	220	230	240
m761.pep	250	260	270	280	290	300
	LKWTGQYTYDNVERTPDRSPTKSVDYDRFGLPYRMGFAHRNDFVKDKLQVWRSDLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPTKSVDYDRFGLPYRMGFAHRNDFVKDKLQVWRSDLEYAFND					
	250	260	270	280	290	300
m761.pep	310	320	330	340	350	360
	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTNDNKTLSNLTNGDYTIGRFE					
a761	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNIAWQQTNDNKTLSNLTNGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

1239

m761.pep	NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
a761	NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
	370 380 390 400 410 420
m761.pep	QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761	QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
	430 440 450 460 470 480
m761.pep	YNKGFAPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTSLAYQIERF
a761	YNKGFAPYGGGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTSLAYQIERF
	490 500 510 520 530 540
m761.pep	NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761	NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
	550 560 570 580 590 600
m761.pep	RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
a761	RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
	610 620 630 640 650 660
m761.pep	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761	LGWNHKNVNVTFAAANLFNQKYWRSDSMPGNPRGYTARVNYRFX
	670 680 690 700

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

m762.seq

1	ATGAAGTGGT	TATTAAATAT	GATAATGAGA	CCTATTAAAT	TTAGTATGGT
51	AAATACGTTA	TTATTTATTG	TTATATGTAG	TTCATTTTTT	GATCTGCTCG
101	TTCAATTATG	TACAATTTTA	TTTCATAGCC	AAAAAATATA	CTTTATTACA
151	TTATTTTTAT	TATTTATTTT	TAATTTTGTT	ACAAAATCTA	TCTATATGGC
201	AATTATTTAT	CCTATTTTAT	ATTTTTTTAC	GATAAAAAAA	TATTATCCTT
251	ACTCTAGGAA	AGTGATAATT	CTATTATCAT	TAGCATTATC	TATATATTTT
301	AGTTTTATGG	ACTTTTACTT	TTTTTCCATA	TATTCAGATA	ACCTTAGCTA
351	TGAAACGGAG	CCTTTACATT	TATACATCCC	TATTATTATT	AATTTTTTCT
401	CACTTTTAGT	TTCTAATTTT	ATTTTATCTT	TTATCAACAA	GTAA

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

m762.pep

1	MKWLLNMIMR	PIKFSMVNTL	LFIVICSSFF	DLLVQLCTIL	FHSQKIYFIT
51	LFLLFIFNFV	TKSIYMAIIY	PILYFFTIKK	YYPYSRKVII	LLSLALSIYF
101	SEMDFYFFSI	YSDNLSYETE	PLHLIPIII	NFFSLVSNF	ILSFINK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

a762.seq

1	ATGAAGTGGT	TATTAAATAT	GATAATGAGA	CCTATTAAAT	TTAGTATGGT
51	AAATACGTTA	TTATTTATTG	TTATATGTAG	TTCATTTTTT	GATCTGCTCG
101	TTCAATTATG	TACAATTTTA	TTTCATAGCC	AAAAAATATA	CTTTATTACA
151	TTATTTTTAT	TATTTATTTT	TAATTTTGTT	ACAAAATCTA	TCTATATGGC
201	AATTATTTAT	CCTATTTTAT	ATTTTTTTAC	GATAAAAAAA	TATTATCCTT
251	ACTCTAGGAA	AGTGATAATT	CTATTATCAT	TAGCATTATC	TATATATTTT

1240

301 AGTTTATGG ACTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA  
 351 TGAACCGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCT  
 401 CACTTTAGT TTCTAATTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

**a762.pep**

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT  
 51 LFLLFIFNFV TKSIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF  
 101 SFMDYFFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK\*

**m762 / a762 100.0% identity in 147 aa overlap**

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDYFFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDYFFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIIINFFSLLVSNFILSFINKX					
	130	140				

**g763.seq not yet found**

**g763.pep not yet found**

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

**m763.seq**

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
 101 CCTATTTTTC CAAATATATC CTACCGGTTT CACTTTTAC CTTGCCACTA  
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
 201 GGGCAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG  
 251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA  
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG  
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG  
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT  
 601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA  
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG  
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC  
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA  
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC  
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA  
 901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA  
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG  
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA  
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC  
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT  
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGCGGCA AGAACGGGTT  
 1201 TTGGAAGACA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACATA  
 1251 CGGCATCCGC AACC GGCTGG AAGTAATACG GGCGCGGAG GAAGTCGCCC  
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACCGG TATTTGCGGA  
 1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

## m763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVAE HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEI AVLAEK QTYENQLNDY TDLD SKQIEA
251 IDTANLLARY LPKLERYS LD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYQYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

## a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGCTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTT CAAATATATC CTACCCGTTT CACTTTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCCGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGTGGG ACAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACAGTT GAACGACTAC ACCGCGCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTGCGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CCGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGCA GCCGTTTGA ACTGAAATCG ACCGAAACCG GCCAACATA
1251 CGGCATCCGC AACCAGCTGG AAGTAATACG GGCGCGCAG GAAGTCGCCC
1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTAGGG TTGGAACCG TATTTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

## a763.pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVAE HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEI AVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYS LD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYQYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          |||||||
a763      MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60

```

1242

	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHV	SANASYQRQPPSISSTRETQ				
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAAFLPHV	SANASYQRQPPSISSTRETQ				
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAEI	IAVLAEKQTYENQLNDY				
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAEI	IAVLAEKQTYENQLNDY				
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKGM	SVGVQLNLPLYTGGELSGKIHEAEA				
a763	QNSRYPTVSAHVGYNLYTSSAQNNNDYHYRGKGM	SVGVQLNLPLYTGGELSGKIHEAEA				
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```

m764.seq
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAAGTACG CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CCGGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGACAGT GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGAAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCCGTGGG GCGGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CCGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGCGA
1001 CCGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTGAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2620; ORF 764&gt;:

```

m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAFLE PAHLELTDTF
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVQGE TLAELEAVGT DSDVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```

a764.seq (partial)
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAAGTACG CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CCGGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGACAGT GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGAAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCCGTGGG GCGGATCGAG CAGCAGAAAA

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1244

```

701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAGG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACGCGGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
  1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
 51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVQKQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

```

m764.pep      10      20      30      40      50      60
MFFSALKSFLSRYITVWRNVWAVRDQLKPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR
|||||
a764          10      20      30      40      50      60
MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR

m764.pep      70      80      90      100     110     120
FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVQKQE
|||||
a764          70      80      90      100     110     120
FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVQKQE

m764.pep     130     140     150     160     170     180
TLAELEAVGTDSDVVQSEQALQAAQLSKRLYEAVLAALESRTVPHIDMAQARSLGLSDAD
|||||
a764         130     140     150     160     170     180
TLAELEAVGTDSDVVQSEQALQAAQLSKRLYEAVLAALESRTVPHIDMAQARSLGLSDAD

m764.pep     190     200     210     220     230     240
VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAEQKLVSVAIEQQKTADYRRL
|||||
a764         190     200     210     220     230     240
VQSAQVLAQHQQYQAWAAQDAQLQSALRGHQAEQKLVSVAIEQQKTADYRRL

m764.pep     250     260     270     280     290     300
RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA
|||||
a764         250     260     270     280     290     300
RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIAAIAQAEQNRVLNTQNLKRDTLDA

m764.pep     310     320     330     340     350     360
LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD
|||||
a764         310     320     330     340     350     360
LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVVAPDD

m764.pep     370     380     390     400     410     420
DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT

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1245

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|||||
a764      DKMDVEVLVLNKDIGFVEQQDAVVKIESFPYTRYGYLTGKVKSVDASHDAVSHEQLGLVYT
              370      380      390      400      410      420

              430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAETIKTGKRRVLDYLLSPLQTKLDESFRERX
              |||||
a764      AVVSLDKHTLNIDGK
              430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT  GCCGTCGGAA  ATCCGTTTGT  GATTTCAGACG  GCATTTTTTTT
51  GAAATTTAAT  TTTTAAAGGA  GTAAACCTAA  ATATGAAATT  TCCTTCCTTC
101 CTTCTTTTAA  ACGGATACTC  TGCCTGTCGG  CAGTAATCTC  GGTATTGGGG
151 GCTTGTGCGG  TCGTTGCTGA  TGTTTACGGT  CATGATTCCG  CCACAATGAA
201 CGCTGCGGCT  GCCAAAGATT  ATATGAAAC  GGTGAGTTA  AACAAAGCTG
251 CCGGCAATGT  CGATACCACA  TCCAGAACAG  CCCGCAGGGT  GCAGGCAGTA
301 TTTTCGACGTA  TGCTGCCTTA  TGCCGATGCG  GCAAATAATA  CCAGCCATAA
351 GTTTGACTGG  AAAATGACGG  TTTTCAAAA  CGATGAGCTG  AACGCGTGGG
401 CAATGCCCGG  TGGAAAAATG  GCGTTTATA  CGGGGATAGT  CGACAAACTC
451 AAGCTGACCG  ATGACGAAAT  TGCCGCCATT  ATGGGGCATG  AATGACGCA
501 CGCCCTGCAT  GAACACGGTA  AAAATAAGGT  CGGGCAGCAA  ATCTTGACCA
551 ATACGGCGCG  GCAGATAGGC  ACGCAGATTA  TATTAGACAA  AAAACCGGAT
601 ACTAATCCGG  AATTGGTTCG  ATTGGGTATG  GATATTTTGG  GGACGTACGG
651 TCTTACCTTG  CCTTATAGCC  GCAGCTTGGA  AGAAGAAGCC  GATGAGGGGG
701 GAATGATGTT  GATGGCGCAG  GCAGGCTATC  ATCCGGCGGC  CGCTGTCAGG
751 GTTTGGGAAA  AAATGAATCA  GGAAAACGAC  CAAAACGGCT  TTATTTATGC
801 TATTACCTCT  ACTCATCCGA  CAAACAATGC  CCGTATAGAA  AATCTAAAC
851 GGTGTGTGCC  GACCGTTATG  CCGGTTTATG  AGCAAAGTGT  CAGAAATAAG
901 GGGCGCGTTA  ATAAAAACG  TCGGCGTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2624; ORF 765&gt;:

```

m765.pep
1  MLRCRPKSVL  DSDGIFLKFN  FLRSKPKYEI  SFLPSFKRIL  CLSAVISVLG
51  ACVVVADVYG  HDSATMNAAA  AKDYMKTVEL  NKSAGNVDTT  SRTARRVQAV
101 FRRLPYADA  ANNTSHKFDW  KMTVFKNDEL  NAWAMPGGKM  AFYTGIVDKL
151 KLTDEIAAI  MGHEMTHALH  EHGKKNVQOQ  ILTNTAAQIG  TQIILDKKPD
201 TNPELVGLGM  DILGTYGLTL  PYSRSLSEEA  DEGGMMLMAQ  AGYHPAAAVR
251 VWEKMNQEND  QNGFIYAIT  THPTNNARIE  NLKRLLEPTVM  PVYEQSVRNK
301 GRVNNKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT  GCCGTCGGAA  ATCCGTTTGT  GATTTCAGACG  GCATTTTTTTT
51  GAAATTTAAT  TTTTAAAGGA  GTAAACCTAA  ATATGAAATT  TCCTTCCTTC
101 CTTCTTTTAA  ACGGATACTC  TGCCTGTCGG  CAGTAATCTC  GGTATTGGGG
151 GCTTGTACGG  TCGTTGCTGA  TGTTTACGGT  CAGGATTCCG  CCACAATGAA
201 TGCTGCGGCT  GCCGAAGATT  ATATGAAAC  GGTGAGTTG  AACAAAGCTG
251 CCGGCAATGT  CGATACTACA  TCCAAAACAG  CCCGTAGGGT  GCAGGCAGTA
301 TTTTCGACGTA  TGTTGCCTTA  TGCCGATGCG  GCAAATAATA  CCGGCCATAA
351 GTTTGACTGG  AAAATGACGG  TTTTCAAAA  CGATGAGCTG  AACGCGTGGG
401 CAATGCCCGG  CGGGAAAAATG  GCGTTTATA  CGGGGATAGT  CGATAAATT
451 AAGCTGACCG  ATGGCGAAAT  TGCCGCCATT  ATGGGGCATG  AATGACGCA
501 TGCCCTGCAT  GAACACGGTA  AAAATAAGGT  CGGGCAGAAA  ATCTTGACTA
551 ATATGGCGCG  GCAGATAGGC  ACGCAGATTA  TATTAGACAA  AAAACCGGAC
601 ACTAATCCGG  AATTGGTTCG  ATTGGGTATG  GATATTTTGG  GGATGTACGG
651 CATTACCTTG  CCTTATAGCC  GCAGCTTGGA  AGAAGAAGCC  GATGAGGGGG
701 GAATGATGTT  GATGGCGCAG  GCAGGCTATC  ATCCGGCAGC  CGCTGTCAGG
751 GTTTGGGAAA  AAATGAATCA  GGAAAACGAC  CAAAACGGCT  TTATTTATGC
801 TATTACCTCT  ACTCATCCGA  CAAACAATGC  CCGTATAGAA  AATCTAAAC
851 GGTGTGTGCC  GACCGTTATG  CCGGTTTATG  AGCACAGTGT  TAGAAATAAG
901 GGGCGCGTTA  ATAAAAACG  TCGGCGTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2626; ORF 765.a&gt;:

```

a765.pep
1  MLRCRPKSVL  DSDGIFLKFN  FLRSKPKYEI  SFLPSFKRIL  CLSAVISVLG

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1246

```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDGEIAAI MGHEMTHALH EHGKKNVQOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSLIEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT STHPTNNARIE NLKRLLPTVM PVYEHSVRNK
301 GRVNKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCR	PKSVL	DSGIF	LKFNFL	RSKPKE	ISFLPS
a765	MLRCR	PKSVL	DSGIF	LKFNFL	RSKPKE	ISFLPS
	10	20	30	40	50	60
	70	80	90	100	110	120
m765.pep	HDSAT	MNAAA	AKDYM	KTVELN	KSAGNV	DTTSRT
a765	QDSAT	MNAAA	AEDYM	KTVELN	KSAGNV	DTTSRT
	70	80	90	100	110	120
	130	140	150	160	170	180
m765.pep	KMTVF	KNDEL	NWAMP	GGKMA	FYTGIV	DKLKL
a765	KMTVF	KNDEL	NWAMP	GGKMA	FYTGIV	DKLKL
	130	140	150	160	170	180
	190	200	210	220	230	240
m765.pep	ILNTA	AQIGT	QIILD	KKPDT	NPELV	GLGMD
a765	ILTNM	AAQIG	TQIIL	DKKPD	TNPELV	GLGMD
	190	200	210	220	230	240
	250	260	270	280	290	300
m765.pep	AGYHP	AAAVR	VWEKM	NQEND	QNGFI	YAITST
a765	AGYHP	AAAVR	VWEKM	NQEND	QNGFI	YAITST
	250	260	270	280	290	300
	310					
m765.pep	GRVNK	KRRRX				
a765	GRVNK	KRRRX				
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCGG TACATTGCCA TCATTTGATC CCTTTGTTAT TGAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTCGAAAT ATCAGGCAAA CTCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGT TTGGAACA GGGCTGTTGC CGGAAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AACTGATGCG GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOEQP GKIEVLEFFG
51  YFCVHCHHFD PLLLKLKAL PSDTYLRTEH VWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FKA VYEOKIR LENRAVAGKW ALSQKGF DGK KLMRAYDSPE  
 151 AAAVALKMQK LTEQY GIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK  
 201 VREERKRQTP AVQK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

## m767.seq

```

1   ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGTCG GGTAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTCTGCGG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTGAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTGTGTCG
301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGAAAACA GGTGCGTTGC CGGAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAACGTATGC GCGCCTATGA TTCCCCCGAA
451 GCTGCCGCCG CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
501 CGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

## m767.pep

```

1   MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
51  YFCVHCHHFD PLLKLKGKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
101 GLKYQANPAV FKA VYEOKIR LENRSVAGKW ALSQKGF DGK KLMRAYDSPE
151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
m767	MMLKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
g767.pep	PLLLKLKGKALPSD TYLRTEHV VWRPEMLGLARMAAAVKLSGLKYQANSV FKA VYEOKIR					
m767	PLLLKLKGKALPSD TYLRTEHV VWRPEMLGLARMAAAVNLSGLKYQANPAV FKA VYEOKIR					
	70	80	90	100	110	120
g767.pep	LENRAVAGKWALSQKGF DGKKLMRAYDSPEAAAVALKMQKLTEQY GIDSTPTVIVGGKYR					
m767	LENRSVAGKWALSQKGF DGKKLMRAYDSPEAAAAALKMQKLTEQYRIDSTPTVIVGGKYR					
	130	140	150	160	170	180
g767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

## a767.seq

```

1   ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AAAACAGTCG GGCAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTCTGCGG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAATTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA
301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGAAAACA GGTGCGTTGC CGAAAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAACGTATGC GCGCCTACGA CTCTCCTGCG

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```

451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCCCAA
601 GTCAGGGAAG AACGAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
1  MKLKHLPLLSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVHCHHFD
51  YFCVHCHHFD PLLKLKGLKALPSDAYLRTEHVWQPEMLGLARMAAAVKLS
101 GLKYQANPAVFKAVYEQKIRLENRSVAEKWALSQKGFQDGLKMRAYDSP
151 AAAAASKMQQLTEQYRIDSTPTVVVGKRYR VIFNNGFDGGVHTIKELVAK
201 VREERKRQTPAVQKX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

```

m767/a767 96.7% identity in 214 aa overlap

a767.pep      10      20      30      40      50      60
MCLKHLPLLSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVHCHHFD
|||||
m767          10      20      30      40      50      60
MCLKHLPLLSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVHCHHFD

a767.pep      70      80      90     100     110     120
PLLLKLGKALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR
|||||
m767          70      80      90     100     110     120
PLLLKLGKALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR

a767.pep     130     140     150     160     170     180
LENRSVAEKWALSQKGFQDGLKMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKRYR
|||||
m767         130     140     150     160     170     180
LENRSVAGKWALSQKGFQDGLKMRAYDSPEAAAAALKMQKLTEQYRIDSTPTVIVVGKRYR

a767.pep     190     200     210
VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
|||||
m767         190     200     210
VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
1  ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
1  MNIKOLITAA LIASAAFATQ AAPQKPVSA QTAHSAVWI DVRSEQEFSE
51  GHLHNAVNI PVDQIVRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCCGC AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT  
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG  
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

**m768.pep**

1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE  
 51 GHLHNAVNIP VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG  
 101 YTNVANHGGY EDLLKKGMMK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

**m768/g768** 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAAPQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLHNAVNIP			
m768	MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHP	AVWIDVRSEQEFSE	GHLHNAVNIP			
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIYEAAAPDKDTPVNLYCRSGRRAEALQEL	KKAGYTNVANHGGYEDLLKKGMMKX				
m768	VDQIVRRIHEAAPDKDTPVNLYCRSGRRAEALQEL	KKAGYTNVANHGGYEDLLKKGMMKX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

**a768.seq**

1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT  
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGGCC CAAACCGCGC  
 101 AACATTACAG CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA  
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG  
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC  
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC  
 301 TATACGAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG  
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

**a768.pep**

1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE  
 51 GHLHNAVNIP VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG  
 101 YTNVANHGGY EDLLKKGMMK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

**m768/a768** 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHS	AVWIDVRSEQEFSE	GHLHNAVNIP			
m768	MNIKHLITAAALIASAAFAAQAPQKPVSAQAQHP	AVWIDVRSEQEFSE	GHLHNAVNIP			
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIHEAAPDKDTPVNLYCRSGRRAEALQEL	KKAGYTNVANHGGYEDLLKKGMMKX				
m768	VDQIVRRIHEAAPDKDTPVNLYCRSGRRAEALQEL	KKAGYTNVANHGGYEDLLKKGMMKX				
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

## g769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTGTA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCCGA ATTGTTGTCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTTCCTATT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GGCGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAACA GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTTCGTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGGG AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
851 AGGTGTGTTT CGGCGGCATC GGTTTTCGCC ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCGACA ATACCCATTT GCAAATTTCC AATTCGCTGG TGTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTTAC CGCGAGCGCA
1151 ACCCGCGCGA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGCGAG AATGGGCGG CAGCGGCCTG TCTTCGCTGT TCCGCCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
1351 CGGGCATTGC ATTTCAAAGG CATCACGCCG CGCCTGACGC TGTCGCACCG
1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

## g769.pep

```

1   LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQGVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAADQFDR LKTEDLPPQL MEQVELYRKA
201 LRERDAWKVN GGFVSTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNWV YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNRWQT PRWQTLSSAE WGRCLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WQEWGSSGL SSLFRLGVAK RHYEKPFFS SFGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

## m769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCTCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGGAATTGAT TGCCGCCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCAGCAT TGTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAAAA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGTGAAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGCGAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTGCGCGACC GGCAGAAAGA TGCCGGGCTG
901 GCAGTGTTC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTTAT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGCGAGTGG GGGCGTTTGA AGAATACGGC CCGGCGCGCT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCAG GAGCGCAACC
1151 CCGCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG GGCCTGTCT TCGCTGTTGC GCCTCGGCGC

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1251

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1251 GGC GAAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

m769.pep

```

1  LIMVIFYFCG KTFMPARNRW MLLPLLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKRQQYG KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRYNG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGGLS SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

	10	20	30	40	50	59
g769.pep	LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLSRPEFRLHEAEVKPI					
m769	LIMVIFY--FCGKTFMPARNRWMLLPLLLASAAYAETPREPDLSRPEFRLHEAEVKPI					
	10	20	30	40	50	
g769.pep	60	70	80	90	100	119
	DREKVPQVREKKGKVLQVDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQD					
m769	DREKVPQVREKKGKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQD					
	60	70	80	90	100	110
g769.pep	120	130	140	150	160	179
	KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAAADQFD					
m769	KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFD					
	120	130	140	150	160	170
g769.pep	180	190	200	210	220	239
	RLKTEDLPQQLMEQVELYRKALRERDAWKVNGGFSVTREHNNINQAPKQQQYGNWTFPKQV					
m769	RLKAENLPPQQLMEQVELYRKALRERDAWKVNGGFSVTREHNNINQAPKQQYQKWTFFPKQV					
	180	190	200	210	220	230
g769.pep	240	250	260	270	280	299
	DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV					
m769	DGTAVNYRLGAEEKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA					
	240	250	260	270	280	290
g769.pep	300	310	320	330	340	359
	GLAVFHERRYGNDAYSYANGARLYFNRWQTPRWQTLSSAEWGRLKNTRRARSNDNTHLQI					
m769	GLAVFHERRYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQI					
	300	310	320	330	340	350
g769.pep	360	370	380	390	400	419
	SNSLVFYRNARQYWTGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGVA					
m769	SNSLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGAA					
	360	370	380	390	400	410
g769.pep	420	430	440	450	460	479
	KRHYEKPFFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE					

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```

m769      KRHYEKPFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTGCGGAT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGGAATTGAT TGTGCGCCAA
451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGCGAGG GTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCCG CGGCATCGGT TTGCGCGACC GCGCGAAAAG TCGCGGCGTG
901 GCAGTGTTC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGCGCGA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGCGAGTGG GGGCGTTTGA AGAATACGCG CCGGCGCGCT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACC GCAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTGTC GCCTCGGCGC
1251 GCGGAAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTAAAGGGG
1301 AAAGGCGCAG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLLPLLASA AYAETPREP DLSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQDDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVMRML AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NOAPKRQYQG KWTFPKQVDG TAVNYRLGAE
251 KKWSLKNWGY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGGSGLS SLLRLGAAGR HYEKPFFSG FKGERRRDKL LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

```

m769/a769  99.8% identity in 490 aa overlap

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQDDKM

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|||||
m769      EKVPQGVREKGVQLIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQDQDKM
              70          80          90          100         110         120

              130         140         150         160         170         180
a769.pep   LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
|||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDPAPAVRMRLAAALFENRQNEAAADQFDRL
              130         140         150         160         170         180

              190         200         210         220         230         240
a769.pep   KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKROQYGKWTFFPKQVDG
|||||
m769      KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKROQYGKWTFFPKQVDG
              190         200         210         220         230         240

              250         260         270         280         290         300
a769.pep   TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
|||||
m769      TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
              250         260         270         280         290         300

              310         320         330         340         350         360
a769.pep   AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRKLNTRRARSNDNTHLQISN
|||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRKLNTRRARSNDNTHLQISN
              310         320         330         340         350         360

              370         380         390         400         410         420
a769.pep   SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLLRLGAAGR
|||||
m769      SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLLRLGAAGR
              370         380         390         400         410         420

              430         440         450         460         470         480
a769.pep   HYEKPFFSGFGKERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYEKN
|||||
m769      HYEKPFFSGFGKERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSDNVFNEYEKN
              430         440         450         460         470         480

              490
a769.pep   RAFVEFNKTFX
|||||
m769      RAFVEFNKTFX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGCGC GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC ACGCGCGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCACGGG GTGCAAGCGG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCCGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKRGTGFA FKSQRIVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGS GIPQTDG VQADTSGKLL AGACIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCTCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSRIQVRY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

```

          10      20      30      40      50      60
g770.pep  MNRLLLLSAAVLP TACGSGETDKIGRASTVFNILGKNDR IEVEGFDDPDVQGVACYISYA
          |||||
m770      MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR IEVEGFDDPDVQGVACYISYA
          10      20      30      40      50      60

          70      80      90      100     110     120
g770.pep  KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKFVKRGTGF AFKSRQIVRY
          |||||
m770      KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKFVKRGTGF AFKSRQIVRY
          70      80      90      100     110     120

          130     140     150     160     170     180
g770.pep  DPKRKAFAYLVYSDKIVQGS PKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI
          |||||
m770      DPKRKTFAYLVYSDKIIQGS PKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
          130     140     150     160     170     180

g770.pep  KNPDKRX
          :| |||
m770      ENLDKRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGC GTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSRIQVRY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

```

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151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFD	DPDVQGVACYISYA
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFD	DPDVQGVACYISYA
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA	VRKPKVEVFKHGASFAFKSRQIVRYY
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA	VRKPKVEVFKHGASFAFKSRQIVRYY
a770.pep	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCF	GGGIPQTDGVQADTSGNLLAGACMISNPI
m770	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCF	GGGIPQTDGVQADTSGNLLAGACMISNPI
a770.pep	ENPDKRX	
m770	ENLDKRX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

```

1  ATGGATTAT  TATCGGTTTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTGGC
51  GGTGCTGACG  ATGCTGCTTT  TGGCGGCAGT  CGGGCTGCAC  GCTTCCGTAT
101  ATCGCACCTT  CACGCCCGAA  AACATCCGCA  GCCGCCTCCA  ACAAGCATT
151  GCCCATACCC  ACCGGAATAT  CTCGTTTGAT  GCGGATATAC  GGCGCAGGCT
201  TCTGCCCCGC  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251  ACGGCGGCCG  GGTGCGCGTT  TCCGTCAAAG  AAACCAAAAT  CGGATTGAGC
301  TGGAAAAACC  TGTGGTCGGA  TCGGATACAG  GTTGAAAAAT  GGGTGGTTTC
351  GGGTGC GGAT  CTTGCCCTGA  CGCGCGACAG  AAACGGCGCT  TGGAACATCC
401  AAGACCTGTT  CGACGGCGCG  AAACACTCCG  CCTCAGTCAA  CCGCATTATC
451  GTCGAAAACA  GCACCGTCCG  CCTCAATTTC  CTGCAGCAAC  AGCTTATCCT
501  GAAGGAAATC  AGCCTCAACC  TGCAATCCCC  CGATTTCGTC  GGGCAGCAGT
551  TTGAAAGTTC  GGGCATACTG  GTTGGAGAA  AGCTGTCCGT  CCCGTGGAAA
601  AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCG  AAATCTCACC
651  GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATCACCATT
701  CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751  GCCGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801  CGCGCAAATC  CCCGCACTGG  CACTCAAAAA  CAACAGCATC  AAAACCGGCA
851  CGGTCAACGG  CACGTTTACC  GCCGGCGGCG  AATATGCCCG  ATGGGACGGT
901  TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951  CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCTT  CAAACCAATT
1001  TCTCCCTCGG  CTCGCCGTTG  GTTGGAGTC  GGGACAACGG  GCTGGACGCC
1051  CCGCGCCTGC  ACATATCGAC  CCTTCAGGAT  ACCGTCGACC  GCCTGCCGCA
1101  ACCCGGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCATA  CCGAATCTGC
1151  AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  ACCCGTTGCC
1201  GCAAAATTC  AATATACGCG  GGAAGGCGCA  CCGCACCTGG  AAGCCGCCGC
1251  CGCGCTGCAA  AAATTAACCC  TCGCCCCCTA  TCTTGACGAA  TTTCGGCAAC
1301  AAAACGGCAA  AATATTCCCC  GACATCCTCG  GCAGGCTGTC  CGGCAACGTC
1351  GAGGCACACC  TCAAAATCGG  CAGCATCCAA  CTCCCCGGCT  TGCAACTGGA
1401  CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGACCATATC  GCGCTCAGCC
1451  GTTTCAGTTC  AGGCTTTTAC  GCGCGCCATA  CCGAAGGCGG  CATCAGCATC
1501  GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAATG  CAAGCAACAT
1551  CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601  GCAACGGCGA  TCGGTCATC  GACCTGACCG  CAAGCGGCGA  AAACCGCAAA
1651  CAGCTTATCC  GCTCGCTGCA  AGGCAGCCTG  TCGCTGAATA  TTCCAACGG
1701  CCGGTGGCAC  GGCATCGATA  TGGACAGCAT  TTTAAAAAAC  GGCCTTCCG

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1256

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1751  GGAAATCTC  GGGCAGCACA  CCCTTCTACC  GATTACGCT  CAACAGCGAA
1801  ATTTAGACG  GCATCAGCCG  CCACATCGAT  ACCGAATCT  TCTCCGACAG
1851  CCTCTATGT  ACCAGCAACG  GCTATACCAA  TCTGGATACG  CAGGAATTGT
1901  CTGAAGATGT  CCTATCCGC  AACGCCGTCC  ATCCGAAAAA  CAAACCGATT
1951  CCCGTAAAA  TCACCGGTAC  GGTGGACAAG  CCGTCCATTA  CCGTCGATTA
2001  CGGCAGGCTG  ACCGGCGGCA  TCAATTCGCG  CAAAGAGAAA  CAGAAAATCC
2051  TCGAAGACAC  CCTGCTGGAA  CAATGGCAGT  GGCTCAAACC  TAAAGAACCG
3051  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1  MDLLSVFHKY  RLKYAVAVLT  MLLLAAVGLH  ASVYRTFTPE  NIRSRLQOSI
51  AHTRKISFD  ADIRRRLLPR  PTVILKNLTI  TEPDGGRRVAV  SVKETKIGLS
101 WKNLWSDRIQ  VEKWVVSAD  LALTRDRNGA  WNIQDLFDGA  KHSASVNRII
151 VENSTVRLNF  LQQQLILKEI  SLNLQSPDSS  GQQFESSGIL  VWRKLSVPWK
201 SRGLFLSDGI  GTPEISPFHF  EASTSLDGHG  ITISTTGSPS  VRFNAGGADA
251 AGLGLRADTS  FRNLHLTAQI  PALALKNNSI  KTGTVNGTFT  AGGEYARWDG
301 SFKLDKANLH  SGIANIGNAE  ISGSFKTPRL  QTNFSLGSPL  VWSRDNLDA
351 PRLHISTLQD  TVDRLPQPRF  ISRLDGSLSI  PNLQNWNAEL  NGTFDRQPVA
401 AKFKYTREGA  PHLEAAAAAQ  KLNLPYLDE  FRQONGKIFP  DILGRLSGNV
451 EAHKIGSIQ  LPGLQLDDME  TYLHADKDHI  ALSRFKSGLY  GGHTEGGISI
501 ANTRPATYRL  QQNASNIQIQ  PLLQDLFGFH  SFSNGDAVI  DLTASGENRK
551 QLIRSLQSSL  SLNISNGAWH  GIDMDSILKN  GLSGKISGST  PFYRFTLNSE
601 ISDGISRHID  TELFSDSLYV  TSNGYTNLDT  QELSEDVLIR  NAVHPKNKPI
651 PLKITGTVDK  PSITVDYGR  TGGINSRKEK  QKILEDTLLE  QWQWLKPKPE
701  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1  ATGGATTTAT  TATCGGTTTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTGGC
51  CGTGCTGACG  ATACTGCTTT  TGCGCGCAGT  CGGGCTGCAC  GCTTCCGTAT
101 ATCGCACCTT  CACGCCTGAA  AACATCCGCA  GCCGCCTACA  ACAAGCATT
151 GCACACACAC  ACCGGAATAT  CTCGTTTGAT  GCGGACATTC  AGCGCAGGCT
201 CCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 GCGGCGACCA  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGCAGGA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAACATCC
401 AAGACTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATATC
451 GTCGAAAAAC  GCACCGTCCG  CCTCAATTTT  CTGCAGGAAC  AGCTTATCCT
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTGCG  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTGGGGGAA  AGCTGTCCGT  CCCGTGAAA
601 AGCAGGGGCG  TGTTCCTTTC  AAACGGCATC  GGCCCGCCCG  AAATCTCACC
651 GTTCCATTTT  GAAGCTTCCA  CTTCGCTGGA  CGGACACGGC  ATTACCATTT
701 CCACCACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751 GCGGCGCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAATC  CCCGCGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTATAC  GCCGGCGGCG  AATATGCCCG  ATGGGACGGT
901 TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCCGCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051 CCGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCGGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCGTGGCC
1201 GCGAAATCA  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCC  GACACCCTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCACC  TGAATAATCG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAAGTC  AGGGCTTAC  GCGCGCCATA  CCGAAGCGCG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAATG  CAAGCAACAT
1551 CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGGCA  CGCGGTATC  GACCTGACCG  CGGGCGGCGA  AACCCGAAAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCACGG
1701 TGCAATGGCA  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751 GCAAACTGCG  CGACAATGCC  GCACCCAGCA  CACCCTTCCA  CCGATTCAAC
1801 CTCAACAGCG  AAATTTTACA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTTCTCCGAC  AGCCTCTATG  TTACCAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCGA  TTCCCTGAA  AATCACCAGG  ACGGTGGACA  AACCTCCAT
2001 TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTTC  CGCAAAGAGA
2051 AACAGAAAA  CCTCGAAGAC  ACCCTGCTGG  AACAATGGCA  GTGGCTCAAA
2101 CCTAAAGAAC  CGTA

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1257

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

```
m771.pep
1 MDLLSVFHKY RLKYAVAVLT ILLLAAGVLH ASVYRTFTPE NIRSRLQOSI
51 ANTHRKISFD ADIQRLLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRRI
151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFSLNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVGQ LPGLQLDDME TYLHADKGGH ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQSSL SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRET
601 LNSEISDGI RHIDTELFSD SLYVTSNGYT NLDTQELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
701 PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

```
m771/g771 90.3% identity in 704 aa overlap
              10      20      30      40      50      60
g771.pep MDLLSVFHKYRLKYAVAVLTMLLLAAGVLHASVYRTFTPENIRSRLQOSIAHNRKISFD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 MDLLSVFHKYRLKYAVAVLTILLAAAGVLHASVYRTFTPENIRSRLQOSIAHNRKISFD
          10      20      30      40      50      60

              70      80      90      100     110     120
g771.pep ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVSGAD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 ADIQRRLPRPTVILKNLTITEPGGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE
          70      80      90      100     110     120

              130     140     150     160     170     180
g771.pep LALTRDRNGAWNIQDLFDGAKHSASVNRIIVENSTVRLNFLQQLILKEISNLQSPDSS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILKEINLNQSPDSS
          130     140     150     160     170     180

              190     200     210     220     230     240
g771.pep GQQFESSGILVWRKLSVPWKSRLGLFSLDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 GQPFESSGILVWGKLSVPWKSRLGLFSLNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
          190     200     210     220     230     240

              250     260     270     280     290     300
g771.pep VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
          250     260     270     280     290     300

              310     320     330     340     350     360
g771.pep SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPLVWSRDGLDAPRLHISTLQD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
          310     320     330     340     350     360

              370     380     390     400     410     420
g771.pep TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFYKTYREGAPHLEAAAAAQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 TVNRLPQPRFISRLDGSLSVPNLQNWNAELNGTFDRQTVAKFYTHEDAPHLEAAVALQ
          370     380     390     400     410     420

              430     440     450     460     470     480
g771.pep KLNLAAPYLDEFQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 KNLNTPYLDDVRQNGKIFPDTLAKLSGDIEAHLKIGKVQLPGLQLDDMETYLHADKGGH
```

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	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRLFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRLFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT					
	:     :     :     :     :     :     :     :     :     :     :     :					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

```

a771.seq
1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101 ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCCGCCTCCA  ACAAGCATT
151 GCCATACGC  ACCGGAATAT  CTCGTTTGAT  GCGGATATAC  AGCGCAGGCT
201 TCTGCCCCG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 GCGGCGACG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAAC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGCAGG  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAACATCC
401 AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451 GTCGAAAAA  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTGCTCG  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601 AGCAGGGGG  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651 GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATTACCATTT
701 CCACACCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751 GCCGCGCTG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAATC  CTTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACG  CGCATTTACC  GCCGCGCGCG  AATATGCCCA  ATGGGACGGT
901 TCGTTCAAA  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCA  TTCGCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGGG
1051 CGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCCGTTT  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCGCCA  AACCGTTGCC
1201 GCGAAATTC  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCT  GACACCTTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCAC  TGAAAATCGG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCCGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAGTC  AGGGCTTTAC  GGCGGCCATA  CCGAAGGCGG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCCTG  CAACAGAATG  CAAGCAACAT
1551 CCAAATCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGCG  CGCGGTATC  GACCTGACCG  CGGGCGGCGA  AACCAGAAAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCAACGG
1701 TGCATGGCAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751 GCAAACTGC  CGACAATGCC  GCACCCAGCA  CACCCCTCCA  CCGATTACAG
1801 CTCACACAG  AAATTTTACA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTTCTCCGAC  AGCCTCTATG  TTACAGCAAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAAT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCG  TTCCCTTGAA  AATCACCAGG  ACGGTGGACA  AACCGTCCAT
2001 TACCGTCGAT  TACGGCAGGC  TGACCGGCGG  CATCAATTCG  CGCAAAGAGA
2051 AACAGAAAT  CCTCGAAGAC  ACCCTGCTGG  AACATGGCA  GTGGCTCAAA
2101 CCTAAGAAC  CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

## a771.pep

```

1  MDLLSVFHKY RLKYAVAVLT ILLLAIGLH ASVYRIFTPE NIRSRLQQSI
51  ANTHRKISFD ADIQRRLLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQILILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTV
401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQONGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGSI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSGNGDAVI DLTAGGETRK
551 ELIRSLQGS SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
601 LNSEISDGI RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEQKILED TLLEQWQWLK
701 PKPEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQQSI	10	20	30	40	50	60
m771	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQQSI	10	20	30	40	50	60
a771.pep	ADIQRRLLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE	70	80	90	100	110	120
m771	ADIQRRLLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE	70	80	90	100	110	120
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILILKEINLNQSPDSS	130	140	150	160	170	180
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILILKEINLNQSPDSS	130	140	150	160	170	180
a771.pep	GQPFESSGILVWGKLSVPWKSRLGLFLSDGIGTPKISPFHFEASTSLDGHGITISTTGSPS	190	200	210	220	230	240
m771	GQPFESSGILVWGKLSVPWKSRLGLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS	190	200	210	220	230	240
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG	250	260	270	280	290	300
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG	250	260	270	280	290	300
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD	310	320	330	340	350	360
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD	310	320	330	340	350	360
a771.pep	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ	370	380	390	400	410	420
m771	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ	370	380	390	400	410	420
a771.pep	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGHI	430	440	450	460	470	480
m771	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI EAHKIGKVQLPGLQLDDMETYLHADKGHI	430	440	450	460	470	480

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	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTNNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTNNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

```

g772.seq
1  GTGTTCCGCA  CGGTCTTGCG  GACTGATGCC  GACTGCCTGC  AAATCATCGT
51  CGTCGGCAAG  TTCTTTCAGG  TTGTTGCGTA  TGGTTTTCGCG  GCGTTGGCGG
101 AAGGCGAGTT  TCACCAAGTTT  GGCAGAAATGA  TCGAAATCGT  CCGCCTTGCC
151 GATACGGTGT  TTCACCGGAA  TCATGCGCAC  CACTGCGGAA  TCGATTTTCG
201 GCGCGGGATC  GAACGATTTCG  GCGGCGACGT  CAATCAGCAG  CTCCATATCG
251 AAAAAATATT  GCAGCATCAC  ACCCAAGCGA  CCGTAGTCGT  TGCTTTTCGG
301 CGCGGCAACC  ATGCGCTCGA  CCCTTCTTT  TTGCAACATA  AAGTGCATAT
351 CGCGGACATC  GTCCGCCACC  TCCGCCAGTT  TGAACAAAAG  CGGCGTGGAG
401 ATGTTATACG  GCAGGTTGCC  GACGATTTTC  TTTTTCGCTG  AGATGCCGTT
451 GAAATCAAAC  TGCAACACGT  CGCCTTCGTG  AATCACCAGT  TTATCCGCAA
501 ACGGCAGCGT  TTTAGACGG  CACACGATGT  CGCGGTCGAT  TTCGACAACG
551 TGCAGCGGT  TCAGCTTTT  CGCCAAAGGT  TCGGTAATTG  CCGCCAAACC
601 CGGGCCGATT  TCAATCACGA  CATCATCCGC  CTGCGGGCGC  ACGGCGTTGA
651 CAATATCGCC  GATAATCCGC  GTGTCCTGCA  AAAAAATCTG  CCCGAAACGC
701 TTGCGGGCTT  TGTGTTCTTT  CATCGTGTTT  CCTCTTCGGT  TGAAACCCCG
751 CCCTTTAGGG  CGGCAGGATC  AGACTCTGTT  TGGGCGGGGC  GTAACCCCTT
801 CCAATCAGG  ACGACACATA  GGGCGGTGCT  TTATGTGTCG  TCCTGTGTGT
851 TGAACATAA  ATGTGTTTAC  AGTATCCGTT  TGATGTCGGC  ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

```

g772.pep
1  VFGTVLRDIA  DCLQIIVVGK  FFQVYVAYGFA  ALAEGEFHQF  GEMIEIVRLA
51  DTVFHRNHAH  HCGIDFRRGI  ERFGRHVNOQ  LHIEKILQHH  TQATVVVAFR
101 RGNHALDHFF  LQHKVHIGDI  VRHLRQFEQK  RRGDVIRQVA  DDFLFA*DAV
151 EIKLQHVAFV  NHQFIRKRQR  FQAYDVAVD  FDNVQAVOLF  RORFGNCRQT
201 RADFNHDIIR  LRAHGVDNIA  DNPRVLQKIL  PETLAGFVFF  HRVSSSVETP
251 PFRAAGSDSV  WAGRNPFQIR  TTHRAVLVYS  SCVLEHKCVY  SIRLMSAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

```

m772.seq
1  ATGTTCCGCG  CGGTCTTGCG  GATTGATGCC  GACTGCCTGC  AAATCATCGT
51  CGCCTGCAAG  CTCTTTCAGA  TTGTTGCGTA  TGGTTTTCGCG  GCGTTGGTGG
101 AAGGCGAGTT  TCACGAGTTT  GGCAAAATGC  TCGAAATCGT  CCGCCTTGCC
151 GATGCGGTGT  TTCACCGGAA  TCATACGGAC  GACGCGGGAA  TCCACTTTCG
201 GCGCAGGGTC  GAACGATTTCG  GCGGTACGT  CAATCAGCAT  TTCCATATCG
251 AAAAAATATT  GCAGCATCAC  GCCCAAGCGG  CCGTAGTCGT  TGCTTTTCGG
301 CGCGGCAACC  ATACGCTCGA  CCCTTCTTT  TTGCAACATA  AAGTGCATAT
351 CGACGACATC  GTCCGCCACC  TCCGCCAGCT  TGAACAAAAG  CGGTGTGGAA
401 ATGTTGTACG  GGAGGTTGCC  GACGATTTTC  TTTTTCGCTG  CGATGCCGTT
451 GAAATCAAAC  TGCAATACAT  CGCCTTCGTG  AATCACCAGT  TTATCCGCAA
501 ACGGCAGCGT  TTTAGACGG  CACACGATGT  CGCGGTCGAT  TTCGACAACG
551 TGCAGCGGT  TCAGCTTTT  CGCCAAAGGT  TCGGTAATCG  CCGCCAAACC
601 CGGGCCGATT  TCAATCACGA  CATCATCCGC  CTGCGGGCGC  ACGGCGTTGA
651 CAATATCGCT  GATAATCCGC  GTGTCCTGCA  AAAAAATCTG  CCCGAAACGC

```



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```

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTTTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep

```

1 MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51 DAVFHRNHTD DGGIHFRRRV ERFGRYVNOH FHIEKILQHH AQAQVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEOK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLYVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHFQ	GEMIEIVRLADTVFHRNHAA				
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
g772.pep	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	DGGIHFRRRVVERFGRYVNOHFHIEKILQHHAQAQVVAFRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
g772.pep	VRHLRQFEQKRGRDVIRQVADDFLAXDAVEIKLQHVAFVNHQFIRKRQRQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD					
	130	140	150	160	170	180
g772.pep	FDNVQAVQLFRQRFNGCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFNGRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
g772.pep	HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTTTHRAVLYVSSCVLEHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLYVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	299

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

```

1 ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTTCTAGA TTGTTGCGTA TGGTTTTGCG GCGTTGGTGG
101 AAGGCAGATT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCC
201 GCGCGGGGTC GAACGATTCT GCGGCAAGCT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGAGCAGTA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTTC TTTTTCCTCG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGCGGCT TCAGCTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATCTG CCCGAAACCG
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GEMLEIVRLA
51 DTVFHRNHAD DGRIHFRRGV ERFGHRVNHQ FHIEEILQHH AQAQVAVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDII RLAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772    95.6% identity in 298 aa overlap

          10      20      30      40      50      60
a772.pep  MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
          |||||
m772      MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
          10      20      30      40      50      60

          70      80      90      100     110     120
a772.pep  DGRIHFRRGVFRFGRHVNHQFHIEEILQHHAAQAVVAFRRGNHTIDHFFLQHKVHIDDI
          |||||
m772      DGGIHFRRRVERFRGVNHQFHIEKILQHHAAQAVVAFRRGNHTLDHFFLQHKVHIDDI
          70      80      90      100     110     120

          130     140     150     160     170     180
a772.pep  VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
          |||||
m772      VRHLRQLEQKRCGNVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
          130     140     150     160     170     180

          190     200     210     220     230     240
a772.pep  FDNVQAVQLFRQRFGNRRQTRTDFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
          |||||
m772      FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
          190     200     210     220     230     240

          250     260     270     280     290     299
a772.pep  HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
          |||||
m772      HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
          250     260     270     280     290
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTTGTGGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAACG CTGATTACGC GCAAATTGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGCTT GTCTGCCAAT
451 GCAAGGTTAC CTAAAAATT TAAACATT TATTATTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTGGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCGCGA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
  1  MGLGATTFVG SGAIGGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
 51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101  TGVKTSLSLTPK TADVQRNLS QSEVGIKWGK GIEGQGPWE DYVGKGLSAN
151  ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGYIDK
201  TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSO
251  NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
  1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
 51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101  CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151  GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201  GGAAATGTTA AACGGGAAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251  CTTCCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301  CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351  CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401  TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451  AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501  GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551  TCAAAGACAG CCAACCGCG CCCGAAGTCA TATTCAAAT CGGCGAATGC
601  CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGAGCCT
651  GATACAGACC TATCCCGGCA GCCCGCGGC AAAACGCGCC GCCGAGCCG
701  TACGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
  1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
 51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDDRKLKE
101  HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151  SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEVIFKIGEC
201  QYRLQOKDIA RATWRSLIQT YPGSPAARKA AA AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
  1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
 51  CTGTGCTTCC GTTTCACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101  CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151  GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201  GGAAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251  CTTCCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAAGAG
301  CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTGAAAC
351  CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401  TTTCTGCCGC TGCCTCCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC
451  AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501  GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551  TCAAAGACAG CCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC
601  CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGAGCCT
651  GATACAGACC TATCCCGGCA GCCCGCGGC AAAACGCGCC GCCGAGCCG
701  TGCGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
  1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
 51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101  HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAAAL LKGADGGDGG
151  SIAQRSMYLL LQSRARMGNC ESVEIGGRY ANRFKDSPTA PEAMFKIGEC
201  QYRLQOKDIA RATWRSLIQT YPGSPAARKA AA AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCASVLPVPEGSRTMPTQENASDGIPYPVPTLQDRLDYLEGKI					
m774	MKIKLPLFIIWLSVSASCASVSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGRITYVQKLDLDRKLKEHYLNTEGGSASAHTVETAQN					
m774	VRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASAHTVETAQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGDGGIAQRSMYLLQLSRARMGNCSVIEIGGRY					
m774	LYNQALKHYKSGKFSAAASLLKGADGGDGGIAQRSMYLLQLSRARMGNCSVIEIGGRY					
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARKRAAAVRRKX					
m774	ANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAARKRAAAVRRKX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

1	ATGAAGACCA	AATTACCGCT	TTTATCATT	TGGCTGTCCG	TATCCGCCGC
51	CTGTCTTCC	CCTGTTTCCC	GCAATATTCA	GGATATGCCG	CTCGAACC GC
101	AGGCAGAGGC	AGGTAGTTCG	GACGCTATTC	CCTATCCCGT	TCCCCTCTG
151	CAAGACCGTT	TGGATTATCT	GGAAGGCACA	CTCGTCCGCC	TGTCGAACGA
201	AGTGGAAACC	TTAAACGGCA	AAGTCAAAGC	ACTGGAGCAT	GCGAAAACAC
251	ACCTTCCAG	CAGGGCATA	GTCCAAAAC	TGCACGACCG	CAAGTTGAAA
301	GAGCATTACC	TCAATACCGA	AGGCGGCAGC	GCATCCGCAC	ATACCGTCGA
351	AACGCACAA	AACCTCTACA	ATCAGGCACT	CAAACACTAT	AAAAGCGGCA
401	GGTTTCTGC	CGCTGCCTCC	CTGTTGAAAG	GCGCGGACGG	AGGCGACGGC
451	GGCAGCATCG	CGCAACGCAG	TATGTACCTG	TTGCTGCAAA	GCAGGGCGCG
501	TATGGGCAAC	TGCGAATCCG	TCATCGAAAT	CGGAGGGCGT	TACGCCAAC
551	GTTTCAAAGA	CAGCCCAACC	GCGCCTGAAG	CCATGTTCAA	AATCGGCGAA
601	TGCCAATACA	GGCTTCAGCA	AAAAGACATT	GCAAGGGCGA	CTTGCGCGAG
651	CCTGATACAG	ACCTATCCCG	GCAGCCCGGC	GGCAAAACGC	GCCGCCGCAG
701	CCGTGCGCAA	ACGATAG			

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

1	MKTKLPLFII	WLSVSAACSS	PVSRNIQDMR	LEPQAEAGSS	DAIPYPVPTL
51	QDRLDYLEGT	LVRLSNEVET	LNGKVKALEH	AKTHPSSRAY	VQKLDLDRKLK
101	EHYLNTGGS	ASAHTVETAQ	NLYNQALKHY	KSGRFSAAAS	LLKGADGGDG
151	GSIAQRSMYL	LLQSRARMGN	CESVIEIGGR	YANRFKDSPT	APEAMFKIGE
201	CQYRLQOKDI	ARATWRSLIQ	TYPGSPAARK	AAAVRRK*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSAACSSPVSRNIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEGT					
m774	MKIKLPLFIIWLSVSASCAS-VSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK					
	10	20	30	40	50	

1265

```
          70      80      90      100     110     120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTEGGSASAHTVETAQ
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGSASAHTVETAQ
          60      70      80      90      100     110

          130     140     150     160     170     180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGDGGGSI AQRSMYLLQLSRARMGNCESVIEIGGR
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      NLYNQALKHYKSGKFSAAASLLKGADGGDGGGSI AQRSMYLLQLSRARMGNCESVIEIGGR
          120     130     140     150     160     170

          190     200     210     220     230     239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQKQDIARATW RSLIQTPGSPA AKRAAAAVRKRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      YANRFKDSPTAPEAMFKIGECQYRLQKQDIARATW RSLIQTPGSPA AKRAAAAVRKRX
          180     190     200     210     220     230
```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```
m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CTTAAACATG GAAACCAAAC CTGTTGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTGAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTGC
551 CCCCCTCGCA GTACACGTTT GCCGTTGCCA TGCCCCGACAC GTCCATGTCC
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TGCGGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCC
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGGTG GAGTCAAAAA ACGGTTTATG TCCGCCGAC AGGCAAGAAG
851 GCGTGTGATG TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTCGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2672; ORF 790&gt;:

```
m790.pep
1  MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTNNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
301 SASKTSTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPV NA*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```
a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CTTAAACATG GAAACCAAAC CTGTTGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTGAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCC
551 CCCCCTCACA ATATACGTTT GCCGTTGCCA TGCCCCGACAC GTCCATGTCC
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TGCGGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCC
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
```

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```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCG GAAGGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAA ACAGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDITI NNHHTHTHNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH ROEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790    98.2% identity in 342 aa overlap

a790.pep      10      20      30      40      50      60
MARRSKTFEEAAEEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
m790          10      20      30      40      50      60
MARRSKTFEEAAEEVEERFGHRGIKLVFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW

a790.pep      70      80      90      100     110     120
GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII
m790          70      80      90      100     110     120
GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV

a790.pep     130     140     150     160     170     180
LNDVQGDITINNHHHTHNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA
m790         130     140     150     160     170     180
LNDVQGDITINNHHHTHNHSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA

a790.pep     190     200     210     220     230     240
SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMRPADEDIVLIELSDKRLVVAHLVID
m790         190     200     210     220     230     240
SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMCPAEDIALIELSDKRLVVAHLVID

a790.pep     250     260     270     280     290     300
IAGRMLIYQTGRPSEALDLPEGSVILGVVLESKNGLCPPHROEGVLIRITAPDVWTVGTI
m790         250     260     270     280     290     300
IAGRMLIYQTGRPSEAFDLPEGSTILGVVLESKNGLCPPHROEGVLIRITAPDVWTVGMI

a790.pep     310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
m790         310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTA CTGTTT
51  TGGTTTGTGT TTTGGTTTTT GTGTATTGG AGTGGGCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCGCT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCGGCGGATG GAGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCGATTTCC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGATGT TTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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```

401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTTGAG TTGTATTTC AATCAGATT AATCCTCGT CAGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCCAAG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAAAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTATCAT AGCTGCCCGG CGGCAGGCGG GTTGCGCTTG
1151 ACAGGCGCGC CTTGGGTTT GCGGCCGAG CGGTGATAA TGAGAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CCGGCGTTGG GCGGTGTTT AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACAGA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCATC GGTGTCGGT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGGAGGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTGATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCCGCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TGCGTGGTTT GTCGGTTT AACCCTGATG GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTGACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CCGGCTGTAT GCTGGACAA
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAAGAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1  MVNYYSAMIK KILTTCEGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAEDKRFY
101 RHWGVDVWVG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNMNLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNNGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRVAV QAMRQPGSTF KPFVYSAAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTFKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVFTA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKGK MKMPEGVVSS NGEYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQQGRSEDT RQDVQETPVL PSNTDSKQQQ
801  LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CCACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACCTGCCG CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGGAAAGCAT
201 CGGTATGTAT GGGGAGCAGC GGCAGCAATT TACAAAAATC GGCGATTTCC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

```

1268

```
451 AATGAGGTGT TGCTTGCCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCCGAT
751 CAGGCGTTGA ATGAGGAAC TGCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCACCCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTGATC CGCGGCAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTCCCCGCC GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCCG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAATAAATG
1201 GGGGAGGACC GTATCCGCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCCGA GCTGTGCGCG CGCTGGTCGG CGGTATGAT
1351 TTTCACAGCA AAACATTCAT TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGCG GCATTATCT AAGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGCG TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGCGAGGCA TATAGCGTAT
1751 TTGCGAACCG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCATATAT ATGTATAAGA
1901 TTATGACGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG TCGGCTACGG CGGTACGATT
2101 CGGGTGCCGG TTTGGGTGGA CTATATGCGT TTGCGTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGCG CTGAAGGTGT GGTACAGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```
1 MVNYYSAMIK KILTTCEGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYLNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMMPA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDRLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPVVTA VYIGFDKPKS MGRVGYGGTI
701 ACPVWVDYMR FALKGKQKKG MKMPEGVVS NGEYYMKERM VTDPLGLTDN
751 SGIAPOPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*
```

g791/m791 97.3% identity in 805 aa overlap

```
10 20 30 40 50 60
g791.pep MVNYYSAMIKKILTTCEGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
|||||
m791 MVNYYSAMIKKILTTCEGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
10 20 30 40 50 60

70 80 90 100 110 120
g791.pep SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
|||||
m791 SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVS
70 80 90 100 110 120
```



1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPPIVNERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPPIVNERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFKVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRRGAVIRVKNNNGRW					
m791	VVLDTTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIIRRGAVIRVKNNNGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPLLGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPLLGALGSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPKGPNQSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI					
m791	KGMTASTVVNDAPISLPKGPNQSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRFPSELPAASLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRFSSELPAASLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGLRLAQMQPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGLRLAQMQPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWVGFNPDVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKQKKG					
m791	TTNDNKDAWVGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVSSNGEYMKERMVTDPLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVSSNGEYMKERMVTDPLTLDNSGIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

## a791.seq

```

1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTC
51  TGGTTTGGTT TTTGGGTTTT GTGTATTGGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCGCT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCGATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTGCTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTATT AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGATTTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGCTGTC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAGT GCATTACGAG CGGTTTGTTC GGAAATCGA
801 TCAGAGTGGT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGTTTAA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAAGAA TATATCGATT
1001 TGAAGTAAGG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAGAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 GGGCGGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGGTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACACAGA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTGCACCTTT AAGCCGTTTG TCTATTGCGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCCG GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCGG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTCGCG CGCCAAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGACGGA TGTGTCCTGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 CCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGCAAGGGGG ATGAAATGCG CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGCG AGCGGCGGGA TGACGAAGTC CGCCAAGATA
2351 TGCAAGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

## a791.pep

```

1  MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMPPA VVLDVTKKKK VVIQLPGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPLQGG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRLLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNNDKDAWF VGFNPVDTVA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALGKQKQKG MKMPEGVVS NGEYMKERM VTDPLGLDLN
751 SGIAPQPSRR AKEDDGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

a791.pep	MVNYYSAMIKKILTTTCFLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	730 740 750 760 770 780

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

**g792.seq**

```

1  ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCCGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAAGAGG CGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAC
451 AGGATTTCG AACTGTATTT AACTCAATC GAATGGCACT ACGGCGtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgcaGACC
551 TGACCAAAAC GCAggcggcG aaactgacgg tactcgtccc cgccccgtt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggt cggcaaatTA ccccaaacgc aaacggactg
701 attgttcag atattgaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

**g792.pep**

```

1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAA KLTVLVPAPF
201 YYSDEPKSKR LRNKTNIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

**m792.seq**

```

1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCCTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCCGAACA GCGGCGAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTG AACTGTATTT AACTCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAAATACCC GCCGCCAAGC
551 TGACCAAAAC GCAGGCGGCA AACTGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

**m792.pep**

```

1  MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAA KLTARVPAPL
201 YYADHPKSKR LRNKTNIVLK RMGSAELPES DTD*

```

**g792 / m792** 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
m792	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASDVR	FAGHGGFDGDGIQNAIRRN	NSGEVKAGGSTISQQLAK			

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m792	WMPYKRISTNLKKALIASEDARFAGHGGSFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK	70	80	90	100	110	120
g792.pep	NLFLNESRNYLRKGEEAAITAMMEAVTDKNRIFELYLNSIEWHYGVFGAEAAASRYFYKKP	130	140	150	160	170	180
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP	130	140	150	160	170	180
g792.pep	AADLTQQAAKLTVLPAPFYSDHPKSKRLRNKTNIVLRRMGSAANYPKAKRTDCSRYGN	190	200	210	220	230	240
m792	AAKLTQQAAKLTARVPAPLYYADHPKSKRLRNKTNIVLKRMGSAELPESDIDX	190	200	210	220	230	
g792.pep	AAXTGVRTAYVFWDLX	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2685>:

```
a792.seq
1  ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CCCCCCATG GAGTGCCTTT ATGTGCGATG GGAAGAAGCA GTTTGAACAG
151 GAAGTCGCGC ATGTGCGCAT GGATTACCGC TGGATTGCCCT ACAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGCGACGG CCGGTTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA CGGGCAAAGT GAAGGCGGGC GGTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCGAAG
401 CGGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTCAC CACAAGAAGC
451 AGGATTTTTG AACTGTATTT AAACCAATC GAATGGCACT ACGGCGTTTT
501 CGGCGGGGAA CGCGCGTCCC GGTATTTTTA TCAAAATACC CGCCGCAAGC
551 TGACCAACAA GCAGCGGGCA AACATGACGG CGCGCGTCCC CGCCGCCGCT
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGCACT
701 GA
```

This corresponds to the amino acid sequence <SEQ ID 2686; ORF 792.a>:

a792.pep

1	MFRIIKWLIA	LPVGIFIFFN	AYVYGNIIY	RAVAPHRTAF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRISTN	LKKALIASED	ARFAGHGDFD	WGGIQNAIR
101	NRNSGKVKAG	GSTISQQLAK	NLFLNESRSY	IRKGEEAAIT	AMMEAVTDKD
151	RIFELYLNSI	EWHYGVFGAE	AASRYFYQIP	AAKLTKQQA	KLTRAVPAPL
201	YYADHPKSR	LRNKTNIIVLR	RMGSAELPES	DTD*	

m792/a792 99.6% identity in 233 aa overlap

		10	20	30	40	50	60
a792.pep		MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792		MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
		10	20	30	40	50	60
		70	80	90	100	110	120
a792.pep		WMPYKRISTNLKKALIASEDARFAGHG GFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK					
m792		WMPYKRISTNLKKALIASEDARFAGHG GFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK					
		70	80	90	100	110	120
		130	140	150	160	170	180
a792.pep		NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP					
m792		NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAAASRYFYQIP					
		130	140	150	160	170	180
		190	200	210	220	230	
a792.pep		AAKLTQQA AKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESD TD X					
m792		AAKLTQQA AKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESD TD X					
		190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2687>:

**g793.seq**

1274

```

1  ATGTTGATTA  AAAGCGAATA  TAAGCCCCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATTAGCTTC  GTCCTGATGG
101 CAATGGCGGT  CTTGTTTGCC  TGTCTGATTG  CCCGCGGGCT  GTATCTGCAG
151 ACGGTAACGT  ATAACTTTTT  GAAAGAACAG  GGCAGCAACC  GGATTGTGCG
201 GACTCAAGCA  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGCGCG  CCGACGGAGT  CCCTGTTTGC  CGTGCCATAA
301 GATATGAAGG  AAATGCCGTC  TGCCGCCCAA  TTGGAACGCC  TGTCGAGCT
351 TGTGATGTG  CCGGTCGATG  TTTTGAGGAA  CAACTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  TTGGATCAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAGCCT  TGGGTTTGGA  AAACTTTGTA  TTTGAAAAAG  AATTAAAACG
501 CCATTACCCG  ATGGGCAACC  TGTTTGACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTCGAAC  TTTGCTTGA  AGACAGCCTG
601 TATGGCGAAG  ACGGCGCGGA  AGTTGTTTTG  CGGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGGACTCCC  CGCGCAATAA  AGCACCGCAA  AACGGCAAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CGGTGCAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGACCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCTGGTTCG  GCAATCAAAC  CGTTCGTGAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA
1001 CGCAGCCTTA  TAAATCGGA  CCGTCTCCCG  TGCGCGATGA  TACCCATGTT
1051 TACCCCTCTT  TGGATGTGCG  CGGCATTATG  CAGAAATCGT  CCAACGTCGG
1101 CACAAGCAAA  CTGTCTGCGC  GTTTCGGCGC  CGAAGAAATG  TATGACTTCT
1151 ATCATGAATT  GGGCATCGGT  GTGCGTATGC  ACTCGGGCTT  TCCGGGGGAA
1201 ACTGCAGGTT  TGTGTGAGAA  TTGGCGCAGG  TGCGGGCCCA  TCGAACAGGC
1251 GACGATGTCT  TTCGGTTACG  GTCTGCAATT  GAGCCTGCTG  CAATTGGCGC
1301 GCGCCTATAC  CGCACTGACG  CACGACGGCG  TTTTGCTGCC  GCTCAGCTTT
1351 GAGAAGCAGG  CGGTTGCGCC  GCAAGGCAAA  CGCATATTCA  AAGAATCGAC
1401 CGCGCGCGAG  GTACGCAATC  TGATGGTTTC  CGTAACCGAG  CCGGGCGGCA
1451 CCGGTACGGC  GGGTGCGGTG  GACGGTTTCG  ATGTCGGCGC  TAAAACCGGC
1501 ACGGCGCGCA  AGTTCGTCAA  CGGGCGTTAT  GCCGACAACA  AACACGTCGC
1551 TACCTTTATC  GGTTTTGCCC  CCGCCAAAAA  CCCCCGTGTG  ATTGTGGCGG
1601 TAACCATCGA  CGAACCGACT  GCCACGGCT  ATTACGGCGG  CGTAGTGCCA
1651 GGGCCGCCCT  TCAAAAAAAT  TATGGGCGGC  AGCCTGAACA  TCTTGGGCAT
1701 TTCCCGGACC  AAGCCACTGA  CCGCCGCGAG  CGTCAAAACA  CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

**g793.pep**

```

1  MLIKSEYKPR  MLPKEEQVKK  PMTSNGRISF  VLMAMAVLFA  CLIARGLYLO
51  TVTYNFLKEQ  GDNRIVRTQA  LPATRGTVSD  RNGAVLALSA  PTESLFAVPK
101 DMKEMPSAAQ  LERLSELVDV  PVDVLRNKLE  QKGKFSFIWK  RQLDPKVAEE
151 VKALGLENFV  FEKELKRHYP  MGNLFAHVIG  FTDIDKGQOE  GLELSLEDSL
201 YGEDGAENVL  RDRQGNIVDS  LDSPRNKAPQ  NGKDIIILSLD  QRIQTLAYEE
251 LNKAVEYHQA  KAGTVVVLDA  RTGEILALAN  TPAYDPNRPQ  RADSEQRNRN
301 AVTDMIEPGS  AIKPFVIAKA  LDAGKTDLNE  RLNTQPYKIG  PSPVRDDTHV
351 YPSLDVRGIM  QKSSNVGTSK  LSARFGAEEM  YDFYHELIG  VRMHSGFPGE
401 TAGLLRNWRR  WRPIEQATMS  FGYGLQLSL  QLARAYTALT  HDGVLLPLSF
451 EKQAVAPQK  RIFKESTARE  VRNLMVSVTE  PGGTGTAGAV  DGFVVGAKTG
501 TARKFVNGRY  ADNKHVATFI  GFAPAKNPRV  IVAVTIDEPT  AHGYYGCVVA
551 GPFFKKIMGG  SLNILGISPT  KPLTAAAVKT  PS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

**m793.seq**

```

1  ATGTTGATTA  AGAGCGAATA  TAAGCCTCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATCAGCTTC  GTCCTGATGG
101 CAATAGCGGT  CTTGTTTGCC  GGTCTGATTG  CTCGCGGACT  GTATCTGCAG
151 ACGGTAACGT  ATAACTTTTT  GAAAGAACAG  GGCAGCAACC  GGATTGTGCG
201 GACTCAAAAC  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGTGGC  CCGACGGAGT  CCCTGTTTGC  CGTGCCATAA
301 GAGATGAAGG  AAATGCCGTC  TGCCGCACAA  TTGGAACGCC  TGTCGAGCT
351 TGTCGATGTG  CCGGTTGATG  TTTTGAGGAA  CAAGCTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  CTGGATTAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAGCCT  TGGGTTTGGA  AAACTTTGTA  TTTGAAAAAG  AATTAAAACG
501 CCATTACCCG  ATGGGCAACC  TGTTTGACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTCGAAC  TTTGCTTGA  AGACAGCCTG
601 CATGGCGAAG  ACGGCGCGGA  AGTCGTTTTG  CGGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGGACTCCC  CGCGCAATAA  AGCCCCGAAA  AACGGCAAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CGGTGCAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGGCCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCCGGTTTC  GCAATCAAAC  CGTTGTGTAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA

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1275

```

1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATG GCGCAGGTGG CGGCCTATCG AACAGCGCAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTCCGT AACCGAGCCG GGCGGCACCG
1451 GTACGGCGGG TCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

**m793.pep**

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIILSLD QRIQTAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNRRRW RPIEQATMSF GYGLQLSLQ LARAYTALH DGVLLPVFSFE
451 KQAVAPQGKR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIAFFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFFKIMGGS LNILGISPTK PLTAAAVKTP S*

```

**g793/m793** 98.5% identity in 582 aa overlap

```

          10      20      30      40      50      60
g793.pep  MLIKSEYKPRMLPKKEEQVKKPMTSNGRISFVLMAIAVLFAACLIARGLYLQTVTYNFLKEQ
          |||
m793      MLIKSEYKPRMLPKKEEQVKKPMTSNGRISFVLMAIAVLFAACLIARGLYLQTVTYNFLKEQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g793.pep  GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSAAQLERLSELVDV
          |||
m793      GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV
          70      80      90      100     110     120

          130     140     150     160     170     180
g793.pep  PVDVLRNKLEQKGKFSIWKRLDPKVAEEVKALGLENFVFEKELKRHPYMGNLFAHVIG
          |||
m793      PVDVLRNKLEQKGKFSIWKRLDPKVAEEVKALGLENFVFEKELKRHPYMGNLFAHVIG
          130     140     150     160     170     180

          190     200     210     220     230     240
g793.pep  FTDIDGKGQEGLELSLEDSLYGEDGAEVVLDRQGNIVDSLSPRNKAPQNGKDIIILSLD
          |||
m793      FTDIDGKGQEGLELSLEDSLHGEDGAEVVLDRQGNIVDSLSPRNKAPKNGKDIIILSLD
          190     200     210     220     230     240

          250     260     270     280     290     300
g793.pep  QRIQTAYEELNKAVEYHQAAGTAVVLDARTGEILALANTPAYDPNRPGRADSEQRNR
          |||
m793      QRIQTAYEELNKAVEYHQAAGTAVVLDARTGEILALANTPAYDPNRPGRADSEQRNR
          250     260     270     280     290     300

          310     320     330     340     350     360
g793.pep  AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIM
          |||
m793      AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRD-THVYPSLDVRGIM
          310     320     330     340     350

          370     380     390     400     410     420
g793.pep  QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS
          |||
m793      QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS
          360     370     380     390     400     410

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1276

	430	440	450	460	470	480
g793.pep	FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE					
m793	FGYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE					
	420	430	440	450	460	470
	490	500	510	520	530	540
g793.pep	PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT					
m793	PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT					
	480	490	500	510	520	530
	550	560	570	580		
g793.pep	AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	AHGYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	540	550	560	570	580	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

a793.seq

1	ATGTTGATTA	AGAGCGAATA	TAAGCCTCGG	ATGCTGCCCA	AAGAAGAGCA
51	GGTCAAAAAG	CCGATGACCA	GTAACGGACG	GATCAGCTTC	GTCCTGATGG
101	CAATAGCGGT	CTTGTTTGCC	GGTCTGATTG	CTCGCGGACT	GTATCTGCAG
151	ACGGTAACGT	ATAACTTTTT	GAAAGAACAG	GGCGACAACC	GGATTGTGCG
201	GACTCAAACA	TTGCCGGCTA	CACGCGGTAC	GGTTTCGGAC	CGGAACGGTG
251	CGGTTTTTGGC	GTTGAGTGCG	CCGACGGAGT	CCCTGTTTGC	CGTGCCCTAAA
301	GAGATGAAGG	AAATGCCGTC	TGCCGCACAA	TTGGAACGCC	TGTCGAGCT
351	TGTCGATGTG	CCGGTTGATG	TTTTGAGGAA	CAAGCTCGAA	CAGAAAGGCA
401	AGTCGTTTAT	CTGGATTAAAG	CGGCAGCTCG	ATCCCAAGGT	TGCCGAAGAG
451	GTCAAAGCCT	TGGGTTTGGG	AAACTTTGTA	TTTGA AAAAG	AATTAAAAACG
501	CCATTACCCG	ATGGGCAACC	TGTTTGACACA	CGTCATCGGA	TTTACCGATA
551	TTGACGGCAA	AGGTCAGGAA	GGTTTGGAAC	TTTCGCTTGA	AGACAGCCTG
601	CATGGCGAAG	ACGGCGCGGA	AGTCGTTTTG	CGGGACCGGC	AGGGCAATAT
651	TGTGGACAGC	TTGGACTCCC	CGCGCAATAA	AGCCCCGAAA	AACGGCAAAG
701	ACATCATCCT	TTCCTCGAT	CAGAGGATTC	AGACCTTGGC	CTATGAAGAG
751	TTGAACAAGG	CGGTCAATAA	CCATCAGGCA	AAAGCCGGAA	CGGTGGTGGT
801	TTTGGATGCC	CGCACGGGGG	AAATCCTCGC	CTTGGCCAAT	ACGCCCGCCT
851	ACGATCCCAA	CAGGCCCGGC	CGGGCAGACA	GCGAACAGCG	GCGCAACCGT
901	GCCGTAAACG	ATATGATCGA	ACCCGGTTCG	GCAATCAAAC	CGTTTGTGAT
951	TGCGAAGGCA	TTGGATGCGG	GCAAAACCGA	TTTGAACGAA	CGGCTGAATA
1001	CGCAGCCTTA	TAAATCGGAA	CCGTCTCCCG	TGCGCGATAC	CCATGTTTAC
1051	CCCTCTTTGG	ATGTGCGCGG	CATCATGCAG	AAATCGTCCA	ACGTCGGCAC
1101	AAGCAAACCTG	TCTGCGCGTT	TCGGTGCCGA	AGAAATGTAT	GACTTCTATC
1151	ATGAGTTGGG	CATCGGTGTG	CGTATGCACT	CGGGCTTTCC	GGGCGAAACT
1201	GCAGGTTTGT	TGAGAAATTG	GCGCAGGTGG	CGGCCTATCG	AACAGGCGAC
1251	GATGTCTTTC	GGTTACGGCC	TGCAATTGAG	CCTGTGTCAA	TTGGCGCGCG
1301	CCTATACCCG	ACTGACGCAC	GACGCGGTTT	TACTGCCGGT	CAGCTTTGAA
1351	AAACAGGCGG	TTGCGCCGCA	AGGC AAAACG	ATATTCAAAG	AATCGACCGC
1401	GCGCGAGGTA	CGCAATCTGA	TGGTTCCCGT	AACCGAGCCG	GGCGGCACCG
1451	GTACGGCGGG	TGCGGTGGAC	GGTTTCGATG	TCGGCGCGAA	AACCGGCACG
1501	GCGCGCAAGT	TCGTCAACGG	GCGTTATGCC	GACAACAAAC	ACATCGCTAC
1551	CTTTATCGGT	TTTGCCCCCG	CCAAAATCC	CCGTGTGATT	GTGGCGGTAA
1601	CCATTGACGA	ACCGACTGCC	CACGGTTATT	ACGGCGGCGT	AGTGGCAGGG
1651	CCGCCCTTCA	AAAAAATTAT	GGGCGGCAGC	CTGAACATCT	TGGGCATTTC
1701	CCCGACCAAG	CCACTGACCG	CCGCAGCCGT	CAAAACACCG	TCTTAA

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

a793.pep

1	MLIKSEYKPR	MLPKKEQVKK	PMTSNGRISF	VLMAIAVLFA	GLIARGLYLQ
51	TVTYNFKLEQ	GDNRIVRTQT	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK
101	EMKEMPAAQ	LERLSELVDV	PVDVLRNKLE	QKGKSFIIWK	RQLDPKVAEE
151	VKALGLENFV	FEKELKRHYF	MGNLFHVIG	FTDIDGKGQE	GLESLSEDSL
201	HGEDGAEEVL	RDRQGNIVDS	LDSPRNKAPK	NGKDIILSLD	QRIQTLAYEE
251	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRP	RADSEQRNR
301	AVTDMIEPGS	AIKPFVIAKA	LDAGKTDLNE	RLNTQPYKIG	PSPVRDTHVY
351	PSLDVRGIMQ	KSSNVGTSLK	SARFGAEEMY	DFYHELIGIV	RMHSGFPGET
401	AGLLRNWRRW	RPIEQATMSF	GYGLQLSLLQ	LARAYTALTH	DGVLLPVSE
451	KQAVAPQGKR	IFKESTAREV	RNLMVSVTEP	GGTGTAGAVD	GFDVGAKTGT
501	ARKFVNNGRYA	DNKHVATFIG	FAPAKNPRVI	VAVTIDEPTA	HGYGGVVAG
551	PPFKKIMGGS	LNILGISPTK	PLTAAAVKTP	S*	

a793/m793 100.0% identity in 581 aa overlap



1277

a793.pep	10	20	30	40	50	60
m793	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
m793	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
m793	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
m793	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
m793	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
m793	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
m793	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
m793	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
m793	490	500	510	520	530	540
a793.pep	550	560	570	580		
m793	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcggtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGTCC GCCGCCCGG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATT CCGAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTGCCG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGG CAGCGGCGAC
451 CCGTTTTCA ATCAGGAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTCGCCG
601 TTTATGACGC CCCAAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 CGCGCGCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTCGGTCAA AAAACTGATG CGCGCATCTT TTTCCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGCCA AAGTTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGT CCGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAAACGG CTTATTTTACG
1251 CCCGTTTGCA CAAGATTTCA TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCGGCGGCG
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

g794.pep

```

1 VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFE YVTDSPMNF
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRMLMD HSLWGEVGSF DHFEADSGSF
201 MTPPNPTML SAGVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILTD MNKRSDNLIA
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDALMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

m794.seq

```

1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGTTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTGCGG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCC AAGCCGACAG CGGTTCGCCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCGTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGGCA AAGTTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCCG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGCGGCGAC GGCAAACTGC CCGCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGT CCGGCTGTG CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAAACGG CTTATTTTACG
1251 CCCGTTTGCA CAAGATTTCA TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGGCG
1501 GATGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

m794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFE YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSVPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLWAGSGD
151 PVFNQENLLD AOKQLREQGI LNITGHLMLD HSLWGEVGGSP DDFEADSGSP
201 FMTPPNPMTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPFA GTDGTLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

```

g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFIMVTIIIIYVISPANKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLL					
m794	VRLNHFIMIAIIIIYVISPANKPARRHSVPTYPALPYNCFYVTDLPMNFPKTAASLLLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g794.pep	ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS					
m794	ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
g794.pep	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRMLMD					
m794	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQQLREQGILNITGHLMLD					
	130	140	150	160	170	180
	190	200	210	220	230	240
g794.pep	HSLWGEVGS PDHFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
m794	HSLWGEVGS PDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
g794.pep	QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	250	260	270	280	290	300
	310	320	330	340	350	360
g794.pep	NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTD MNKRSDNLIA RSVFLKLGGD					
m794	NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTD MNKRSDNLIA RSVFLKLGGD					
	310	320	330	340	350	360
	370	380	390	400	410	420
g794.pep	GKLPVSEQAASAVRRELAVSGIDVADLVL ENGSGLSRKERVTARMAQMLETAYFSPFA					
m794	GKLPVSEQAASAVRRELAVSGIDVADLVL ENGSGLSRKERVTARMAQMLETAYFSPFA					
	370	380	390	400	410	420
	430	440	450	460	470	480
g794.pep	QDFIDTLPFA GTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGDKPM AVVVIINSGR					
m794	QDFIDTLPFA GTDGTLRNRFKQSGGLRLKTGT LNNVRALAGYWLGDKPM AVVVIINSGR					
	430	440	450	460	470	480
	490	500	510			
g794.pep	AVSLLPDLN FVAKNIISGGDGWLDKLMCKERRAX					
m794	AVSLLPDLN FVANNIISGGDGWLDKLMCKERRAX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```

a794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTAT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC

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1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGGCAGC AATTACCGCT GGGCGACCGA GTTAAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCGG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTTCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAAC TCGGCGCGAC GGCAAAC TGC CCGCGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGT GAAACCGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCAGCAATG TTGGAACCG CTTATTTACG
1251 CCGGTTTGCA CAAGATTTCA TCGATACGCT GCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGGCGCGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAAGGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

## a794.pep

```

1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLV TFAAFKTFGS NYRWATEFES NGTVNDGTL DNLWAGSGD
151 PVFNQENLL VQRQLREQGI RNITGHLMLD HSLWGEVGS DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAOTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLV ENGSGLSRKE
401 RVTARMMQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLNNVRL AGYWLGDKEP AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

```

a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIA	IIIYVISPAN	KPARRHSVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
m794	VRLNHFIMIA	IIIYVISPAN	KPARRHSVPT	YPALPYNCF	YVTDLPMNFP	KTAASLLLLL
	10	20	30	40	50	60
a794.pep	ASLAHALDT	GRIPONEIAV	YVQELDSGKV	IIDHRSDVP	VNPASTMKLV	TFAAFKTFGS
m794	ASLAHALDT	GRIPONEIAV	YVQELDSGKV	IIDHRSDVP	VNPASTMKLV	TFAAFKTFGS
	70	80	90	100	110	120
a794.pep	NYRWATEFES	NGTVNDGTL	DNLWAGSGD	PVFNQENLL	AVQRQLREQ	GI RNITGHLMLD
m794	NYRWATEFES	NGTVNDGTL	DNLWAGSGD	PVFNQENLL	DAQQLREQ	GI RNITGHLMLD
	130	140	150	160	170	180
a794.pep	HSLWGEVGS	PDDEFADSG	SPFMTPPNP	TMLSAGMVM	VRAERNAAD	STDILTDPPLPHIFA
m794	HSLWGEVGS	PDDEFADSG	SPFMTPPNP	TMLSAGMVM	VRAERNAAG	STDILTDPPLPHIFA
	190	200	210	220	230	240
a794.pep	QNNLKITASQ	AACPSIKKLM	RASFSDNTLK	LRGNIPESCL	GKPVGVRMFA	LDELIRQSFT
m794	QNNLKITASQ	AACPSIKKLM	RASFSDNTLK	LRGNIPESCL	GKPVGVRMFA	LDELIRQSFT
	250	260	270	280	290	300
a794.pep	NHWLLGGGRI	SDGIGISDTP	EGAOTLAVAH	SKPMKEILTD	MNKRSNLI	ARSVFLKLGGD
m794	NHWLLGGGRI	SDGIGISDTP	EGAOTLAVAH	SKPMKEILTD	MNKRSNLI	ARSVFLKLGGD
	310	320	330	340	350	360
a794.pep	NHWLLGGGRI	SDGIGISDTP	EGAOTLAVAH	SKPMKEILTD	MNKRSNLI	ARSVFLKLGGD
m794	NHWLLGGGRI	SDGIGISDTP	EGAOTLAVAH	SKPMKEILTD	MNKRSNLI	ARSVFLKLGGD

1281

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|||||:|||||:|||||
m794      NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDNKRSDNLIARSVFLKLGGD
           310      320      330      340      350      360

           370      380      390      400      410      420
a794.pep   GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
           |||||||
m794      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
           370      380      390      400      410      420

           430      440      450      460      470      480
a794.pep   QDFIDTLPIAGTDGTLRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
           |||||||
m794      QDFIDTLPIAGTDGTLRNRFKQSGGLRLKTGTLNNVRALAGYWLGDKPMVAVVVIINSGR
           430      440      450      460      470      480

           490      500      510
a794.pep   AVSLLPDLDNFVANNIISGGDGWLDKLMCKERRAX
           |||||||
m794      AVSLLPDLDNFVANNIISGGDGWLDKLMCKERRAX
           490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

```

g900.seq
1   ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATCGC GCGCTTCTTT GCGCGCTTTT TGCGCGcctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TCGGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCGCCTCG
251 CCCCAGGCCA AGCCGTCGGC AAGCATTGTC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTCTGT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCTG
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 gggccggcAa tgtcgcgcgc cATTtgcacg tgttgGATTT GGTCCGCCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCTGTC
701 CCGTTTTCCG CATTTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCCTC GGGGTCCAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tgGGTGGATT GGTGAATCAT
901 CTCTTGCTCG TGGCATTGA TGATGCCGTG GTAATCGGCG AGGAAGAGGA
951 AGGATTTCGT ATCGGGGTTT TCGCCCGCGC GGACGGCGGG GCGGATGCGC
1001 CCGACGTAGT TGCCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAaA. gatgCGCCGA TTATACCCGA TTGCCACAT ACATCCAGCC
1151 GacaACagaC TTTTCCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng>:

```

g900.pep
1   MPSEMPSETW QAEVRTALGL FORADADRIA YFIQQFARFF ARFLRACLQN
51  LFDLRRIRGQ CVVAFAQFCQ FGVDfRRRKf FRLAPSQAVG KHLRkFRFRf
101 RRGEgFIDfK QRAfVGLfRL ARLfHVGNdf VDRfLGfFfVv fPKRngIAvG
151 FGHFASVQTD QEFdVfVdfH FGQGEeFLET VGEAAGNVAR HFDVLDLVAP
201 DGDFVGVEHQ NVGSHQNRIT EQTHfHTEIG VFLPVfFRIGL NGGFVGVGAV
251 HQTlGGDAGQ NPVQLHHfGN VALAVEGGAL GVESAGKPSG GNGLGGLVNh
301 LLLVAFDDAV VIGEEEGfGf IGVLRRADGG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPsEREK DAPIIPDLPH TSSRQQTfPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

```

m900.seq
1   ATGCCGTC TG AAACGCGGCA GGCGGAGGTT CGGACGGCAT CGGGTTCATT
51  TCAACGGGCG GATGcCGACC GCATCgG.TA CTTGTGCCAA TAATTGCGGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTTG

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1282

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CGGCGTTGAT TTTCGCGGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TGGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGCGAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGCGATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCC GTTTTCTGCA
701 TTTGCTGCA CGGCGCTTT GTAGGCATGG GCGCGGTCA TCAAACCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGT
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTGCGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGC GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCGGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```

m900.pep
  1 MPSETRQAEV RTASGSFQRA DADRIXFVQ *FACFFTRFR RACLQNLFDL
 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPCR NGVAVGFHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTAIRVFLP VFCICLHGGF VGMGAVHQT
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHRLRV
301 AFDDTVVIGE EEEFGGIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QOTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```

m900/g900

      10      20      30      40      50
m900.pep  MPSETRQAEVRTASGSFQRADADRIGYFVQXFACFFTRFRACLQNLFDLRRVGGQ
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ
          10      20      30      40      50      60

      60      70      80      90     100     110
m900.pep  LVVAFARFGEFGVDFFRQKFFGFTPRQAVGKHFRKFHRFRRRGEFGVDFKQWAFVGLFRL
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      CVVAFAQFCQFGVDFFRRKFFRLAPSAVGKHLRKFRRFRRRGEGFIDFKQRAFVGLFRL
          70      80      90     100     110     120

      120     130     140     150     160     170
m900.pep  ARLFHIGDDFVDRFLGFFVFPKRNGVAVGFGHFASVQTDQEFVDFIDFHFGQGEEFPEA
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      ARLFHVGNDFVDRFLGFFVFPKRNGIAVGFGHFASVQTDQEFVDFVDFHFGQGEEFLET
          130     140     150     160     170     180

      180     190     200     210     220     230
m900.pep  VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFICL
          | |||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900      VGEAAGNVARHFDVLDLVAPDGDVVGVEHQNVGSHQNRITEQTHFHTIGVFLPVFRIGL
          190     200     210     220     230     240

```

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	240	250	260	270	280	290
m900.pep	HGGFVGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	:      :      :      :      :      :					
g900	NGGFVGVGAVHQTLGGDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	250	260	270	280	290	300

  

	300	310	320	330	340	350
m900.pep	LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL					
	:      :      :      :      :					
g900	LLLVAFDDAVVIGEEEEFGFIEVLRRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL					
	310	320	330	340	350	360

  

	360	370	380
m900.pep	AASMPSEREKDVPIIPDLPTSSRQQTFFPYX		
	:      :      :		
g900	TAAMPSEEREKDAPIIPDLPTSSRQQTFFPYX		
	370	380	390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900.seq (partial)

```

1   GAGGTTCGGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51  CACGTACTTT GCCCAATAAT TCGCGTGCTT CTTTACGCGC TTTTTCGCGC
101 CCTGCCTGCA AAATCTCTTC GATTTGCGAA GGGTCGCGCG TCAGCTCGTT
151 GTAGCGTTCG CGCGGTTTCG CGAGTTCGGC GTTGATTTTC GCCGCCAAAA
201 GTTTTTTTGC CTCGCCCAA GCCAAGCCGT CGGCAAGCAT TTTCGTAAT
251 TCTGCCGTTT CAGACGCGCT GGAGAAAGCT TTGTAGATTT CAAACAGAGG
301 GCTTTCGTCG GGCTTCTTCG GCTCGCCCGG CTCTTTCATA TTGGTGATGA
351 TTTTGTGTGAC CGATTTTGGG GTTTTTTGTG CGTTTCCCA AAGCGGAATG
401 GTGTTGCCGT AGGATTGGGA CATTTTGCGT CCGTCCAAAC CAACCAAGAG
451 TTCGACGTTT TCGTCGATTT TCACTTCGGG CAGTGTGAAG AGTTCCTGGA
501 AGCGGTGGTT GAAGCGGCCG GCAATATCGC GTGCCATTTC AACGTGTTGG
551 ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601 GGCAGTCATG AGGATAGGGT AGCTGTACAA ACCCATTTCC ACGCCGAAAT
651 CGGGGTCTTC CTGCCGTTT TCCGCATTG CCTGCACGGC GGCTTTGTAG
701 GCGTGGGCGC GGTTTCATCA ACCCTTGCGG GTGATGCAGG TCAGAAATCCA
751 GTTCAATTCC ATCACTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801 GCTCGGGGTC GAGTCCGCAG GCAAGCCAAG TGGCGCAAC GGCTTGGGTG
851 GATTGGTGAA TCATCTCCGG CTCGTGGCAT TTGATGATAC CGTGGTAATC
901 GGCGAGGAAG AGGAAGGATT CGGTATCAGG GTTTTGCGCC GCGCGGACGG
951 CGGGGCGGAT AGCAGCGACG TAGTTGCCCA GATGCGGGAT GCCGTGGGTG
1001 GTTACGCCGG TCAGAACTCG TTTTGTGCTC ATAAAAATGT CCTGCGGCA
1051 TCAATGCCGT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTGACC
1101 ACCTACATCC AGCCGACAAC AGACTTTTCC ATATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900.pep (partial)

```

1   EVRTALGLEFQ RADTDRITYF AQ*FACFFTR FLRAQLQNLFLDLRRVGGQLV
51  VAFARFGEFG VDFRRQKFFC LAPSQAVGKH FRKFCRFRRR GESFVDFKQR
101 AFVGLLRRLAR LFHIGDDFVD RFLGFFVVFV KRNGVAVGFG HFASVQTNQE
151 FDFVDFHFG QCEEFPEAVV EAAGNIACHF NVLDLVATDW NFMGIEHENV
201 GSHEDRVAVQ THFHAIEGVE LPVFRICLHG GFVGVGAVHQ TLGGDAGQNP
251 VQFHHFGNVA LTVEGGALGV ESAGKPSGGN GLGGLVNHRL LVAFD DTVVI
301 GEEEEFGFIR VLRRADGGAD STDVVAQMRD AGGGYAGQNS FFAHKNVLAA
351 SMPSEREKDA PIIPDLPTS SRQQTFFPY*

```

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900.pep	MPSETRQAEVRTASGSFQRADADRIXFYVQXFACFFTRFLRAQLQNLFLDLRRVGGQLVVA					
	:      :    :   :					
a900	EVRTALGLEFQRADTDRITYFAQXFACFFTRFLRAQLQNLFLDLRRVGGQLVVA					
	10	20	30	40	50	
	70	80	90	100	110	120

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```

m900.pep    FARFGEFGVDERRQKFFGFTPRQAVGKHFRKFHRRRRGEGFVDFKQWAFVGLFRLARLF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        FARFGEFGVDERRQKFFCLAPSQAVGKHFRKFHRRRRGESFVDFKQRAFVGLLRLARLF
              60          70          80          90          100         110

              130         140         150         160         170         180
m900.pep    HIGDDFVDRFLGFFVVFPRNGVAVGFGHFASVQTDQEFDFIDHFGQGEFPEAVVEA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        HIGDDFVDRFLGFFVVFPRNGVAVGFGHFASVQTNQEFDFVDFHFGQCEEFPEAVVEA
              120         130         140         150         160         170

              190         200         210         220         230         240
m900.pep    AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
||::| ||:||||| | :||:|||||:|||||:|||||:|||||:|||||:|||||
a900        AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
              180         190         200         210         220         230

              250         260         270         280         290         300
m900.pep    VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNLRLV
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNLRLV
              240         250         260         270         280         290

              310         320         330         340         350         360
m900.pep    AFDDTVVIGEEEEFGIEVLRRADGGADGVVAQMRDAGGGYAGQNSFFAHKNVLAASM
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        AFDDTVVIGEEEEFGIRVLRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
              300         310         320         330         340         350

              370         380
m900.pep    PSEREKDVPIIPDLPTSSRQQTFFPYX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900        PSEREKDAPIIPDLPTSSRQQTFFPYX
              360         370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCGATT TTCGATGTC CAATTGGGCC GTTGCCCTTT CCATCACATT
51  GGCTGCCCGT TTGTTTACCG TATTAGyAG TGGCTTGGTG ATGTTTTCCTA
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGGCGGT
151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG
401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGCCCGA GCCGTTGGGG
601 GCGGCTTTGG GCTATTTGGT TTTCAGCCG TTTTGTTCGC CTGCCGTGTT
651 TGGTTCGGTA TTCGCGTGA TAGCCGGTGT GATGGTGT TTGGCGTTGG
701 ACGAGCTGnt GCCGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
751 TACGGCTGA CAACGGGTAT GCGGCTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2706; ORF 901&gt;:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSGLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP

```



1285

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN  
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG  
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV  
 251 YGLTGMMAVI AVSLVLFHF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

## a901.seq

1 ATGCCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCCTTT CCATTACGTT  
 51 GGCTGCCGCT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTCCA  
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGGCGGT  
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC  
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTCGCGCG GCGACCATGG  
 251 CATTTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG  
 301 AACCCGCATG AAACCTTTAGA CGCGCAAGAC CCGTCGTTC AAGAAAGCAA  
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG  
 401 CGCACAATT CCCTCAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT  
 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC  
 501 GGAGGGCATT TCCATCGCG CGCCGGTTTA TTTTGGCCAC CGCAGCCGTA  
 551 AGAAAACGCT GTGGGCGTGT CTGCTATCCG GCTTGCCCGA GCCGTGGGG  
 601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTGTGCG CTGCCGTGTT  
 651 TGGTTTCGTA TTCGGCGTGA TAGCCGCTGT GATGGTGTTT TTGGCGTTGG  
 701 ACGAGCTGCT GCCGCTGCC AAACGCTATT CAGACGCCA TGAAACCGTT  
 751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT  
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

## a901.pep

1 MPDFMSNLAVAFSITLAAGLFTVLGSGLV MFSKTPNPRVLSFGLAFAGG  
 51 AMVYVSLTEI FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVP  
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN  
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG  
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV  
 251 YGLTGMMAVI AVSLVLFHF\*

m901/a901 98.9% identity in 269 aa overlap

	10	20	30	40	50	60
m901.pep	MPDFMSNLAVAFSITLAAGLFTVLGSGLV MFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
a901	MPDFMSNLAVAFSITLAAGLFTVLGSGLV MFSKTPNPRVLSFGLAFAGGAMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
a901	FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
	70	80	90	100	110	120
m901.pep	FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
a901	FSKSSEAF AEIYDKDHAF AAATMAFLAGMG GIALIDRLVP NPHE TLDAQD PSFQESKRRH					
	130	140	150	160	170	180
m901.pep	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA					
a901	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
	190	200	210	220	230	240
m901.pep	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA					
a901	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
	190	200	210	220	230	240
m901.pep	KRYSDGHETV YGLTGMMAVI AVSLVLFHF					
a901	KRYSDGHETV YGLTGMMAVI AVSLVLFHF					
	250	260	270			
m901.pep	KRYSDGHETV YGLTGMMAVI AVSLVLFHF					
a901	KRYSDGHETV YGLTGMMAVI AVSLVLFHF					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCCTG AACCCTGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTGATTTC
151 ACGCCGCGCC TGTTGCGCGT GGGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GCGCGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GCGCGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTTGGT CTCGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcgG CGcgcccgtg aacggcaaGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgctcgtcg tgccaaccca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCCTGC
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCttgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcgg
801 catCCGCCAT CtgttcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTTGCGA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQN GGS AFCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAIIF GDFGDGGQVL
201 IVVVPQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDL RPE SDVVTRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCA ACTGTGCGTT TTTTCGGCAA GTCTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTGCGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTGTTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGCG GATGAGTTCT TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCCTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTGCGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTGATAAAA ATAGCCGCGG ATGTGCATAA TGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep

```

1  LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51  CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFCQTQGRR
101 QNTVFGIMFQ IAEEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRKCDGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT CLFAVGHF				
g902	10	20	30	40	50
	MPSEPERRHGNTALPFP I AARPTVGFGSGKPKITGKCVLRRRIVQAVDFTPRLFAVGHF				
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHTGGVAVKRVY GADVQNSGGAFCQTQGRRQNTVFGIMFQIAEEPRPA				
g902	60	70	80	90	100
	ADVPAVFACDAHTDGLTIKRVHGADVQNGGSAFCQTQGRRXNAVFGIMLQIAEKPRPA				
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
g902	120	130	140	150	160
	LRAAPYHDAVGGGLFEDGGGFLRRSDVAVDPGRDVQTAFGLGDEFVTRLAFVHLRARAPV				
m902.pep	180	190	200	210	220
	DGKGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFGQNGGNQRLV LHQRATGL				
g902	180	190	200	210	220
	NGKGGNAIFGDFGDDGQVLIVVVPTQTGFEGNGYARRLDHRLQNGGNQRLV LHQRATGL				
m902.pep	240	250	260	270	280
	DIADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSIS				
g902	240	250	260	270	280
	DVAHFLGGAAHIDVDDL RPESDVVTRIRHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
m902.pep	300	310	320	330	340
	ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLY				
g902	300	310	320	330	340
	ERRIAGQHFAHRPTCAKRPT EAAEGFVGNARHRRKCDGVVDKITADVHNGPAFQKSAPLY				
m902.pep	360				
	IFX				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTCAAG ATAACCTGCA

```

1288

```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTCG CCGTCGGGCA TTTCGTGCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAAACTCA AGGCAGGCGG
301 TAAAACACCG TGTTGCGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTC CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTGCGTG CGCGTGCCTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGCGCAT TTTGCGCATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACGCG CTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTG CGCACACCGC CCAACCTGCG CCAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

```

a902.pep
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLR RTVQAVDFTT
51 CLFAVGHEVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGR
101 *NTVFGVMFQ IAEPRSALR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFHR PTCAKISAKS AERFVGNARH RRCDDGVVDK IADVHNGSA
351 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCS	EGIWAVGARPT	VGFFGKSFKIT	CKHVVLRRT	TVQAVDFTT	CLFAVGHEVD
a902	LHFQRIIKCS	EGIWAVGARPT	VGFFGKSFKIT	CKHVVLRRT	TVQAVDFTT	CLFAVGHEVD
	10	20	30	40	50	60
	70	80	90	100	110	120
m902.pep	VPAYVFACDA	HTGGVAVKRV	YGADVQNSG	GAFCQTQGR	RQNTVFGIM	FQIAEPRPALR
a902	VPAYVFACDA	HTGGVAVKRV	HGSDVVQNS	GTFQQTQGR	XNTVFGVMF	QIAEPRSALR
	70	80	90	100	110	120
	130	140	150	160	170	180
m902.pep	AAPYHNAVGG	GLFEDGLGFL	RRSNVAVDP	DRDVQTA	FGFGDEFV	TRFAFVHLR
a902	AAPYHNAVCG	GLFEDGLGFL	RRGNVAVDP	DRDVQTA	FGFGNQV	SRFAFVHLR
	130	140	150	160	170	180
	190	200	210	220	230	240
m902.pep	KGGDAAI	FGDFGDDG	QVLMVVVPT	QTGFEGNG	YACRTDDG	FQNGGNQRL
a902	KGGNAAI	FGDFGDDG	QVLMVVVPT	QTGFEGNG	YARRFDHR	LQNGGNQRL
	190	200	210	220	230	240
	250	260	270	280	290	300
m902.pep	ADFFSGTAH	VDVKLRPKA	DDVTRGIRH	LLRIASGNL	HGNNAAFI	GKIAAVQGF
a902	ADFFSGTAH	VDVKLRPKA	DDVTRGIRH	LLRIASGNL	HGNNAAFI	GKIAAVQGF
	250	260	270	280	290	300
	310	320	330	340	350	360
m902.pep	RVAGQHFAH	RPTCAKISA	KSARFVGN	ARRRRCDD	GVVDKIAA	ADVHNGSA

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```

          |||
a902      RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep    X
            |
a902        X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51 TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCGGgt
101 tTGCCTTcaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAACTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgtttc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAc GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTc AGCCCTTTTc
751 GGTAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCCG CTTC AACCGC CTGTTGTATC GTGATGCCAA ACCGAAAACC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAGT ACTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTCCCAACA AGGATATATC GGTCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCTTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAAGTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAACTCT AGCCGGCACA GCAATTGGGA
1451 TACCGGGCA GATAAAGCTT GCGGCAACC TGCAATACGA TATATTTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatttt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL LNLRLDLEOGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGSL DMFYVNYGRS IGGTPDEENF DGRHKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTR TKS YIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTFPQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYL GAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWVTGFO VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51 CCGTTTCGAG CAACCATTTG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTG GGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTTCTAATC TTCGCGATGT AGAGCAGGGC TTGGAAGAAC TCGCTCGTTT
501 GCCCGAGTGT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCACT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCTTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
701 TTTATATATG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAG CTGAAAGCGG ATCCAGAAAGT TACAGCGTGC ATTATTCTGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTATCCGA ACCATCAGTT CTATCTCGGT GCGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNKFLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNVDYNGKQ
301 YQSSLAER LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGDI LPGTSRMKII
401 TASLDAAAPF XLGKQFFYA TAIQAQWNKT PLVAQDKLSI GSRVTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

              10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
              |||  |||  |||  |||  |||  |||
g903      MATQVGGANSDEASPCFPISEVELVGEETAKFRFALNHA
              10      20      30

              70      80      90      100     110     120
m903.pep  MKETAFKTMCLGSNNLSRLQKAAQILIVRGYLTSAIIQPQNMDGILKLRVSAGEIG
              :  :  |  :  |  ||  :  :  :  :  :  ||  ||  ||  :  :  ||  :  :  |  :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRYTTTRILAAPQDLNSGKQLTLMPGYLR
              40      50      60      70      80      90

```

		130	140	150	160	170	180
m903.pep		DIRYEKKRDGKSAEGSSISAFNNKFPLYRNKILNLRDVEQGLLENLRRPLSVKTDIQIIPSE					
		:    : : :   : :     :             :   :       :         : : : : :   :   :					
g903		SIRIDRSNDDQTHAGRIAAAFQNKFPTRSNDDLNLRLDLEQGLLENLKLCLPTAEADLQIVPVE					
	100	110	120	130	140	150	
		190	200	210	220	230	
m903.pep		EE-GKSDLQIKWQQNK-PIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDLFYVSYGR					
		:  : :   : : : :   :   :   : : :           : : :       :       :     :					
g903		REPQNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFYVNYGR					
	160	170	180	190	200	210	
		240	250	260	270	280	290
m903.pep		GLAHKTDLTDATGTETESGSRYSVHYSVPVKKWLFSFNHNGHRYHEATEGYSVNYDYNG					
		: : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :					
g903		SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNHNGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270	
		300	310	320	330	340	350
m903.pep		KQYQSSLAERMLWRNRLHKTSVGMKLWTRQTYKYIDAEIEVQRRRSAGWEAELRHAY					
		:   : : : : :   :   : : : :   :   :   :   :   :   :   :   :   :   :					
g903		KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDDAELTVQRRKTTGWLAELSHKGY					
	280	290	300	310	320	330	
		360	370	380	390	400	410
m903.pep		LNRWQLDGLKLSYKRGTMGRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFF					
		: :       :   :   :   :   : : :   :   :   :   :   :   :   :   :					
g903		IGRSTADFKLKYKHGTGMKDALARAPEEAFGE--GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390	
		420	430	440	450	460	470
m903.pep		YATAIQAWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFY					
		: : :           : :     :   : : :           :   :   :   :   :   :					
g903		YDTSVHAQWNKTPLTSSQDKLAIGGHHTVRGFDGEMSLPAERGWIYWRNDLSWQFKPGHQLY					
	400	410	420	430	440	450	
		480	490	500	510	520	530
m903.pep		LGADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
		:   :   :   : : :     : : :   :   :   :   :   :   :   :					
g903		LGADVGHVSGQSAKWLSGQTLAGTAIGIRGQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510	
		540					
m903.pep		YGFNLNYSFX					
		: :					
g903		TGFQVGYSFY					
		520					

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAAC TG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTTCTTCC	TTCTGTGCTC	ATGAAAAGAA	CAGCTTTTAA
201	AAC TGGGATG	TGTTAGGTT	CCAATAATT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTC	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATTC	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCCGCATGT	AGAGCAGGGC	TTGGAAAAAC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAGGAAGGCA
551	AAAGCGATTG	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTTCAGT

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601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAG CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCCGTAATA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

## a903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51  RKFSFLPSVL MKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNKFLYRNK
151 ILNLRDVEQG LENLRRRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERM LWRNRFHKTS VGMKLWTRQT KYIDDAEIE VQRRRSAGWE
351 AELRHRLAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPGTSRMKII
401 TAGLDAAAPF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

## m903/a903 98.4% identity in 547 aa overlap

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL					
a903	MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA RKFSFLPSVL					
	10	20	30	40	50	60
m903.pep	MKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG					
a903	MKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG					
	70	80	90	100	110	120
m903.pep	DIRYEEKRDG KSAEGSISAF NNKFLYRNK ILNLRDVEQG LENLRRRLPSV KTDIQIIPSE					
a903	DIRYEEKRDG KSAEGSISAF NNKFLYRNK ILNLRDVEQG LENLRRRLPSV KTDIQIIPSE					
	130	140	150	160	170	180
m903.pep	EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL					
a903	EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL					
	190	200	210	220	230	240
m903.pep	AHKTDLTATGT ETESGSR SYSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ					
a903	VHKTDLTDATGT ETESGSR SYSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ					



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	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKT SVGMK L WTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKT SVGMK L WTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRG TGMRQ SMPAPEENG GDILPGT SRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRG TGMRQ SMPAPEENG GGTIPGT SRMKIITAGLDAAAPFMLGKQQFFYA					
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTNTVYG					
	550	560	570	580	590	600
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

```

g904.seq
1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGC GCGCCTT CAAACAGCAG TTTTCGCCG TTTTGTGTTT
651 TTTCTGTTCA CACGCGggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTGTCTTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCTG
901 GCCGATTTTG CTTTGCCGCG GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAAGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTGCGCGCG
1151 ACGACCAAGG TATGGCCGCG ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

```

g904.pep
1  MMQHNRRFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```

m904.seq

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

m904.pcp

1	MMQHNRFSSV	GAGGDDGDRR	AADFFNPFI	CFGVFGQCAV	VLHAESGFAP
51	AGHGFVNRLA	GFHRIGTARQ	DVGFAAVGQF	IADADIDGFN	AVHYIEFSNT
101	HTGNAVDLDG	AFQGGGIKPA	AAACASGYRT	EFVSAFCQTY	AYFVEQFGRE
151	RARTDARGIG	FDDAQNI IQH	LRTYARACRS	CARQTVGRGN	EGISAVVDVQ
201	QRTLRAFQKQ	FFAVFVFLVQ	HAGHVGNHRR	NARRDFFDNR	HHVFRFNRLG
251	IVQMLQLDIV	IGKDGIOFFT	QFXRMQIGG	ANGAACHFVF	VGRADAAAAGR
301	ADFAFAAXIF	AGLVERDVVR	QDQRAGRND	QTAFDVGHAC	RVQLVDFAQQ
351	GFGGDNPART	DEAVQTVMQD	AARNAQNGF	FAADNQGMAR	IVAALAEAHHA
401	AGFFRQPVND	FTFTLVAPLC	ADXNIFSHS	HITYRY*	

Homology with a predicted ORF from *N. gonorrhoeae*

m904/q904

	10	20	30	40	50	60
m904.pep	MMQHNRFFSVGAGGDDGDRRAADFFNPFI					
	:                               :     :   :     :					
g904	MMQHNRFFAVGAGGDDGDRRAADFFNPFI					
	10	20	30	40	50	60
	70	80	90	100	110	120

1295

m904 . pep	GFHRIGTARQDVGFAAVGGQFIADADIDGFNAVHYIEFSNTHTGNAVDLDGAFQGGGIKPA
g904	GFHRIRRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNAVDLDGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAAAAAGYRTEFVSALRQTCAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	CARQTVGRGNEGISAVVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
g904	RAGETVGRGNEGVSAVVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
	190 200 210 220 230 240
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDGIIQFFTFQFXRMQQIGGANGAACHFVFVGRADAAAGR
g904	HHVFRFNRSQVMQVLELDVVGKDGIIQFFTFQFXRMQQIGGANGAACHFVFVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	ADFAFAARIFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFQAQGGFGGDDNART
g904	ADFAFAARCFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFQAQGGFGGNDNART
	310 320 330 340 350 360
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAALAHHAAGFFRQPVNDFTFTLVAPLC
g904	DEAIQSFVQDTARNQAQNGFFAADDQGMARIVAALAHDAAGFFRQPVNDFTFTLVAPLC
	370 380 390 400 410 420
m904 . pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTCGCTCCA
151	ACCGGGCATG	GTTTCGTAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTCAAC	GCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACCGACC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGGCCT	ACGCCGCGC	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGTFTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGT	AATGCGCGGC
701	GCGACTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

**a904 . pep**

```

1 MMQHNRFFAV GAGGDDGDRR TADFFNPFQI CFGIGR*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDLG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFHRLG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*

```

**m904/a904 91.3% identity in 436 aa overlap**

	10	20	30	40	50	60
m904 . pep	MMQHNRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA					
a904	MMQHNRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVAFAHAESGFAPTGHGFVNRLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m904 . pep	GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTHGTNAVLDLGAFFQGGGIKPA					
a904	GFYRIRAARQDVGFAAVGQFVADADIDGFNAVHYIEFGNTHGTNAVLDLGAFFQGGGIKPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m904 . pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIQHRLTYARACRS					
a904	AAACASGYRTEFVSAFCQTCSDFEQFGRERARTDARGIGFDDAQNIQHRLRAYARACRS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m904 . pep	CARQTVGRGNEGISAVVDVQRTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR					
a904	RAGEAVGRSNEGVS AVVDVQRTLRAFQKQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQQIGGANGAACHFVFGVGRADAAAGR					
a904	HHVFRFHRLGIVQMLQLDVVISKDGIOFFTQFFRMQQIGGANGAACHFVFGVGRADAAAGR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m904 . pep	ADFAFAAXIFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFAQQGGGDDNART					
a904	ADFAFAARCF SGLVERDVIRQDQRAGRRDFQTAFDVFHACRVQLVDFAQQGGGDDNART					
	310	320	330	340	350	360
	370	380	390	400	410	420
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQGMTRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
	370	380	390	400	410	420

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```

m904.pep      ADXYNIFSHSHITYRYX
              || ||||| ||||| |||
a904          ADYYNIFSHSHITXRYX
              430

```

g906.seq not found yet  
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT
51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTCGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTCTGCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
51  SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51  GTTGTGTGCC GCCGGTGCCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCTGCC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGTTAT GCCGTTkTGG AAAAActACA TCGGCAAACC GGCGCACAAC
451 CTGTTGACCA TCCGCACCAA CCGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLLSPLA HAGAQREETL ADDVASVMRS
51  SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```

1298

151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW  
201 RNRWQWR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPEDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
	:	:	:	:	:	:
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
g907.pep	RARIIS					
m907	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHRYNLEKGNIVRAL					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

```

1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCTT
51  ATTGTGTGCT GCCGGCGCGC TGTGTGCTCAG CCCGCTGGCA CAAGCCGGCG
101 CGCAACGTGA AGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC
151 TCTGTCGGCA GCATAAATCC GCCGAGGCTG GTGTTCGACA ATCCGAAAGA
201 GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCGTCC
251 CCGATGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTTGG AAAAATAACA TCGGCAAACC GGCGCACAA
451 CTGTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCGTTTGA
551 ACGGTAGCCT CGGCAGCAAT AAATATCCGA ACGCCGTTTT GGGCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

```

1  MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAQREETL ADDVASVMRS
51  SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

```

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL					
	:	:	:	:	:	:
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDVASVMRSSVGSINPPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	:	:	:	:	:	:
a907	VFDNPKEGERWLSAMSARLARFVPEDEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m907.pep	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
	190	200				
m907.pep	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTTCGCA GGTGTAAGT CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPTQTAT LFPIIREQVK PDSIVYTDY RSYDVLVDSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSQYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTVPTQTAT LFPIIREQVK PDSIFYTDY RSYDVLVDRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10      20      30      40      50      60
g908.pep  MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXLIYQNGPHLEMF

```

1300

	:           :             :                 :                 :
m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNTAAYFYHRLRLLIYQNSPHLEMF
	10 20 30 40 50 60
	70 80 90 100 110 120
g908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
m908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK
	70 80 90 100 110 120
	130 140 150 160
g908.pep	PDSIVYTDCYRSYDVLDVSEFSHFSFAETSFSYQSQHTFCRTTKPYX
m908	PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX
	130 140 150 160

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2739>:

```

a908.seq
1  ATGAGAAAAA  GTCGTCTAAG  CCAGTATAAA  CAAAATAAAC  TCATTGAGCT
51  ATTTGTGCGCA  GGTGTAACGT  CAAGAACGGC  AGCAGAGTTA  GTAGGCGTTA
101  ATAAAAATAC  CGCAGCCTAT  TATTTTCATC  GTTTACGATT  ACTTATTTAT
151  CAAAACAGTC  CGCATTTTGA  AATGTTTGAT  GCGCAAGTAG  AAGCAGATGA
201  AAGTTATTTT  GGCGGACAAC  GCAAAGGCAA  AGCGGGTCGC  GGTGCTGCCG
251  GTAAAGTCGC  CGTATTCGGT  CTTTTGAAGC  GAAATGGTAA  GGTTTATACG
301  GTTACAGTAC  CGAATACTCA  AACCGCTACT  TTATTTCCTA  TTATCCGTGA
351  ACAAGTGAAA  CCTGACAGCA  TTGTTTATAC  GGATTGTTAT  CGTAGCTATG
401  ATGTATTAGA  TGTGCGCGAA  TTTAGCCATT  TTAGCTTCGC  TGAAACTTCG
451  TTTTCGTATC  AATCACAGCA  CACATTTTGC  CGAACGACAA  AACCATATTA
501  A

```

This corresponds to the amino acid sequence <SEQ ID 2740; ORF 908.a>:

**a908.pep**

1	MRKSRLSQYK	QNKLIELFVA	GVTARTAAEL	VGVNKNTAAY	YFHLRLLLIY
51	QNSPHLEMF	GEVEADESYF	GGQRKGKRGR	GAAGKVAVFG	LLKRNGKVYT
101	VTPNTQTAT	LFPIIREQVK	PDSIVYTDCY	RSYDVLDVRE	FSHFSFAETS
151	FSYQSQHTFC	RTTKPY*			

**m908/a908** 98.2% identity in 166 aa overlap

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLI	ELFVTGVTARTAAEL	LVGVNKNTAAYYFH	RLRLLIYQNSPH	LEMFD	
a908	MRKSRLSQYKQNKLI	ELFVAGVTARTAAEL	LVGVNKNTAAYYFH	RLRLLIYQNSPH	LEMFD	
	10	20	30	40	50	60
	70	80	90	100	110	120
m908.pep	GEVEADESYFGGQR	KGKRGRGAAGKVAV	FGLLKRNGKVYTV	VPNTQTATLFPII	REQVK	
a908	GEVEADESYFGGQR	KGKRGRGAAGKVAV	FGLLKRNGKVYTV	VPNTQTATLFPII	REQVK	
	70	80	90	100	110	120
	130	140	150	160		
m908.pep	PDSIFYTDCYRSYD	VLVDVREFSHFSFA	ETSFSYQSQHTFC	RTTKPYX		
a908	PDSIVYTDYRSYD	VLVDVREFSHFSFA	ETSFSYQSQHTFC	RTTKPYX		
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2741>:

```
g909.seq (partial)
      1  atgcgtaaaa ccgtaacttat cTgaccatc tccgcgcgcc ttttgtcggg
     51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
    101  caaaatgttc caccggcacg cgcgtgtgtt ggcaagacgg gcgcggctcg
```



1301

```

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtggtgcg
201 caaccaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggcgagg gacggggggg ggcggtgaa cagggcagaa
301 acgggggagg ggaagcgatc ggcgagg..

```

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

```

1 MRKTVLILTI SAALLSGCTW ETYQDGS GKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLRNQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEKRSAR..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

```

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AACCAAAGTT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

```

1 MRKTFLEFLTA AAALLSGCAW ETYQDGN GKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTAAAAALLSGCAWETYQDGN GKT AVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
		:	:	:	:	:
g909	MRKTVLILTI SAALLSGCTW ETYQDGS GKT AVRACSTGT PLCWQDGRGS KKVDCDEYGG					
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQT GNNADEEHRQ HWQKPKFQNRX					
	:		::	:	:	:
g909	ERRAVLRNQKRGKPTRRAATLGKPSFRARDGGGRVNRAETGEGKRSAR					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

```

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTGTGCGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AGCCCAAATT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

```

1 MRKTFLEFLT AAALLSGCAW ETYQDGN GKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

```

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTAAAAALLSGCAWETYQDGN GKT AVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
		:	:	:	:	:
a909	MRKTFLEFLTAAALLSGCAWETYQDGN GKT AVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQTGNNADEEHRQHWQPKPFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQPKPFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCCG
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLSAAAFAFAG DSAERQIYGD PHFEQNRKA VKMLEQRGYQ
51  VYDVDADDDH GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

g910/m910

	10	20	30	40	50	60
g910.pep	MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRKAVKMLEQRGYQVYDVDADDYW					
	: : :					
m910	MKKLLLAADVSLSAAAFAFAGDSAERQIYGDPHFEQNRKAVKMLEQRGYQVYDVDADDDH					
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
m910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

a910.pep

1303

1 MKKLLLVAVV SLAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ  
51 VHDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR\*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLA	AVVSLS	AAAFAG	DSAERQ	IYGD	PHFEQNRTKAVKMLEQRGYQVYD
a910	MKKLLLV	AVVSLS	AAAFAG	DSAERQ	IYGD	PYFEQNRTKAVKMLEQRGYQVHDVDADDHW
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLE	VEAYK	DGREY	DIVLS	YPD	LKIIKEQLDRX
a910	GKPVLE	VEAYK	DGREY	DIVLS	YPD	LKIIKEQLDRX
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq  
1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG  
51 CGCGGCGGCG GTTGCCTTTC TCGCTTCCG CGTGGCGGGC GGCGCGGCGT  
101 TCGGCGGTTT GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC  
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG  
201 GCGGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC  
251 GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA  
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG  
351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT  
401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC  
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep  
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI  
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ  
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA  
151 EKNADGGNAE KAAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq  
1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG  
51 CGCGGCGGCG GTTGCCTTTC TCGCTTCCG CGTGGCGGGC GGTGCGGCGT  
101 TCGGCGGTTT GGACAAAAC TACGCCGTTT ATGCCGATTT CGGCGACATC  
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG  
201 GCGGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC  
251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA  
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG  
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT  
401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC  
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep  
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI  
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ  
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA  
151 EKNADGGNAE KAAE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10	20	30	40	50	60
----	----	----	----	----	----

1304

```

g911.pep      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
|||||
m911          MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
              10      20      30      40      50      60

              70      80      90      100     110     120
g911.pep      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
|||||
m911          SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
g911.pep      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEKNAEKAEX
|||||
m911          ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1   ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGAAGTTCG TCCTGATTGG
51  CGCGCGGCG GTTGCCTTTC TCGCTTCCG CGTGCGCGG GGTGCGCGGT
101 TCGGCGGTTT GGACAAACT TACGCCGTT ATGCCGATT CGGCACATC
151 GCGCGTTTGA AGGTCAATGC CCGCGTCAA TCCGCAGGC TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATTG GGACGGCAAG TATCAGTTC GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGC TGACGAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCA CACCATCTCC GTAACAGTT
401 CTGCAATGGT TCTGAAAAC CTTATCGGC AATTCATGAC GAGTTTTGCC
451 GAGAAAAATG CCGACGGCG CAATGCGGA AAAGCCGCC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1   MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK  SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

**m911/a911** 100.0% identity in 164 aa overlap

```

              10      20      30      40      50      60
m911.pep      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
|||||
a911          MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
              10      20      30      40      50      60

              70      80      90      100     110     120
m911.pep      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
|||||
a911          SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
              70      80      90      100     110     120

              130     140     150     160
m911.pep      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
|||||
a911          ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1   gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

```

151 CGCCCAAAG CCGAAGCCTA TCGGGTCCC TATTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG TACCGCGTCC GACGCGCAAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTCAA AAACGCGACC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAGGGCGGCA AGGAAATCGT CGTCCGTGCC GAAGTCGGCA
401 TCCCCGGTCA GAAGCCCGTC AATATGGACT TTACCACCTA CCAAAGCGGC
451 GGCAAATACC GTACCTACAA CGTCGCCATC GAAGGCACGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATCAT CAAAGCCAAA GGCATCGACG
551 GGCTGATTGC CGAGTTGAAA GCCAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:

```

g912.pep
  1 VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQATQVLT ILKSGDAASA
 51 RPKAEAYAVP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTY
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTYR NQFGEI IKAK GIDGLIAELK AKNGGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2761>:

```

m912.seq
  1 ATGAAAAAAT CCTCCCTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
 51 CCGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAGCCAA ATCCGTCAAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA ACGGCGATGC CAACACCGCT
151 CGCCAAAAG CCGAAGCCTA TCGGATTCCC TATTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGTGGACG
551 GACTGATTGC CGAGTTGAAA GCCAAAACG GCGGCAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:

```

m912.pep
  1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA
 51 RQKAEAYAIP YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTY
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEI IKAK GVDGLIAELK AKNGGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

```

g912/m912

      10      20      30      40      50      60
g912.pep  VKKSSFISALGIGILSIGMAFASPADAVGQIRQATQVLTILKSGDAASARPKAEAYAVP
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912      MKKSSLISALGIGILSIGMAFAAPADAVSQIRQATQVLSILKNGDANTARQKAEAYAIP
          10      20      30      40      50      60

      70      80      90     100     110     120
g912.pep  YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKFKNATVNVKDNPIVN
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912      YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKNANVNVKDNPIVN
          70      80      90     100     110     120

     130     140     150     160     170     180
g912.pep  KGGKEIVVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTYR NQFGEI IKAK
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m912      KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYR NQFGEI IKAK
          130     140     150     160     170     180

          190
g912.pep  GIDGLIAELKAKNGGKX

```

1306

m912                   |:|||||||||||||  
                       GVDGLIAELKAKNGGKX  
                                   190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq  
 1 ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTGAGCAT  
 51 CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA  
 101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC  
 151 CGCCAAAAAG CCGAAGCCTA TGCATTCC CATTTCGATT TCCAACGTAT  
 201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAA  
 251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC  
 301 GGCACGATGC TGAAATTA AAACGCCAAC GTCAACGTCA AAGACAATCC  
 351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG  
 401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC  
 451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC  
 501 CGTGATCCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCGTGGACG  
 551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pep  
 1 MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA  
 51 RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYTS  
 101 GTMLKLKLNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG  
 151 GKYRTYNVAI EGASLVTYR NQFGEI IAK GVDGLIAELK AKNGSK\*

m912/a912 98.0% identity in 196 aa overlap

	10	20	30	40	50	60
m912.pep	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP					
	:                 :             :					
a912	MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP					
	10	20	30	40	50	60
m912.pep	70	80	90	100	110	120
	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKLNANVNVKDNPIVN					
	:                 :             :					
a912	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLKLNANVNVKDNPIVN					
	70	80	90	100	110	120
m912.pep	130	140	150	160	170	180
	KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEI IAK					
	:                 :             :					
a912	KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNVQFGEI IAK					
	130	140	150	160	170	180
m912.pep	GVDGLIAELKAKNGGKX					
	:					
a912	GVDGLIAELKAKNGSKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq  
 1 atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC  
 51 CCCTGCATTG GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC  
 101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCT  
 151 GCCGCGCGCG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT  
 201 GTCCAATTTT TTTAACAACC TGCGCGACGT GGTCAGTTTC GGCAGCAATA  
 251 TCTTGCGTTT GGAcatCAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc  
 301 atCAATACCA CCTTCGGTTT GGgcgGGCTC ATTGATATTG CCGGcgcGGg  
 351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG  
 401 GctgGAAaa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc

```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcgttttc cataccctg cgggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctctctgatt tgaccgacag TCtggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTC CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
  1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVTP KPVVRAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWGTT AAAAVSTREG LLDLTDLSLE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
251 PAVHEDSVSE TQAEAGEAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
  1 ATGAAAAAAA CCGCCTATGC CTTCTCTCTG CTGATCGGGT TCGCTTCCGC
 51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTC AAC GACCAAGCCG ACCGCTACAT TTTCCGCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTACAGTTC GGCAGCAATA
251 TCTTGCCTT GGACATCAAA CGCGCAAGCG AAGACCTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTGGG CGACACGTTT GCCTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTGTC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCTG TCGGACGCTG GGGCAGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGgtACGGAA GATAACATCG
701 ACATCGACGA ATTGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
  1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
 51 AARGYRKVAP KPVVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDLSLE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETO PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

```

g913/m913
      10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYEGYNRAVSKFNDQADRYIFAPAARGYRKVTP
          |||::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
m913      MKKTAYAFLLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP
          10      20      30      40      50      60

      70      80      90     100     110     120
g913.pep  KPVVRAGVSNFFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
m913      KPVVRAGVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP
          70      80      90     100     110     120

```

1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCTCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCCGCGCGCG GCTACGCAA AGTTGCGCCG AAACCCGTCC GCGCCGCGGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCACTTC GGCAGCAATA
251 TCTTGCGCTT AGACATCAA CGCGCAAGCG AAGACCTTGT CCGGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGA AAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCTG TCGGACGCTG GGGCAGGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGC GCGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVEKFN DQADRYIFAP
51  AARGYRKVAP KPV RAGVS NF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AAI DKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVEKFN DQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVEKFN DQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPV RAGVS NF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGL IDIAGAGGIP					
a913	KPV RAGVS NF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGL IDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					



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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTTCG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLW
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTTCGACGAT TTTTTCGACC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTGTATGT TTTTGGGCAG GTCGATTGCG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TGCGGGTCAG
651 GAACATTTTC ATTTGTTCGG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
701 TGATATGCGC GTTGTAGCGT CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEDA
101 IRCRKFDXCI GWTDKETDTD TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

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151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFP DLMFLGRSIW  
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRISDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEDEAIRCRKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSPLDFPCIGFQTALEQCSCSADSXASTIFCTRGCRRTSSPVKVKYSPATP					
m914	TELGFRLCFSPLDFPCIGFQTALEQCSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

1	ATGAAAAAAT	GTATTTTGGG	CATTTTGACC	GCGTGTGCCG	CCATGCCTGC
51	ATTTGCCGAC	AGAATCGGCG	ATTTGGAAGC	ACGTCTGGCG	CAGTTGGAAC
101	ACCGTGTGCG	CGTATTGGAA	AGCGGCAGCA	ATACCGTCAA	AATCGACCTT
151	TTCGGTTCAA	ATTCCACCAT	GTATGTATGC	AGCGTTACGC	CTTTTCAGAA
201	GACGTTTGAG	GCAAGCGATC	GGAATGAAGG	CGTGGCGCGG	CAGAAAGTGC
251	GTCAGGCGTG	CAACCGCGAA	ACTTCGGCAA	TGTTTTCGCA	AGATGAGGCA
301	ATCCGATGCA	GAAAATTCGA	TTGATGTATC	GGTTGGACGG	ATAAAGAAAC
351	GGATACGGAG	CTTGGCTTCC	GTATCTGTTT	TTCTCTGCCC	GATTTTCCAT
401	GCATCGGGTT	TCAGACGCGA	TTGGAATGTC	AGTCGTGTTT	TGCCGATTCT
451	TAGGCTTCGA	CGATTTTTCG	CACCAAAGGA	TGCCGACAAA	CGTCTTCGCC
501	GGTAAAGGTG	TGGAAATACA	GCCCTTCCAC	GCCGTGCACT	TTCTCACGCG
551	CATCTTTTAA	TCCCCGATTG	ATGTTTTTGG	GCAGGTCGAT	TTGGCTGGTG
601	TCGCCGGTAA	TGACGGCTTT	CGCGCCGAAG	CCGATGCGGG	TCAGGAACAT
651	TTTCATTTGT	TCGGGCGTGG	TGTTTTGCGC	TTCGTCGAGG	ATGATGTATG
701	CGCCGTTGAG	CGTCCTGCCG	CGCATATAG		

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

1	MKKCILGILT	ACAAMPAFAD	RIGDLEARLA	QLEHRVAVLE	SGSNTVKIDL
51	FGSNSTMYVC	SVTPFQKTFE	ASDRNEGVAR	QKVRQACNRE	TSAMFCEDEA
101	IRCRKFD*CI	GWTDKETDTE	LGFRICFSLP	DFPCIGFQTA	LECQSCSADS
151	*ASTIFCTKG	CRTTSSPVKV	WKYSPSTPCS	FSRASFPNDL	MFLGRSIWLV
201	SPVMTAFAPK	PMRVRNIFIC	SGVVFCASSR	MMYAPLSVLP	RI*

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m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGFRICFSLPDFPCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTL					
a914	TELGFRICFSLPDFPCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMFLGRSIWLSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1 ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51 CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2778; ORF 915.ng&gt;:

g915.pep

```

1 MKKTLLAIVA VFALSACROA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51 KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGC.tG
51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCcCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACATATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

Computer analysis of this amino acid sequence gave the following results:

ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLLAIVAVSALSXCRAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLLAIVAVSALSACRAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPWFSTIKQMFGYTKLPEEPKIRVIYVTDMGNVTDWTNPADTEWMDAKKAFYVIDS					
a915	DQPWFSTIKQMFGYTKLPEEPKIRVIYVTDMGNVTDWTNPADTEWMDAKKAFYVIDS					

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgccagc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGCAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GCGCGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGCG GCATTGAAGT TTATGGTGGC
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNG IKVTYDVYDS DETLESKVL T GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLNTAKRR AEEAGGKEKI RVMPKKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGCCAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGCAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

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1314

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751  GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801  GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851  ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901  TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951  CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCTAT CCAGCCGCGC GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```

1  MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKNG IKVTYDVYDS DETLESKVLTKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLK QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDLNIAKRR AEEAGGKEKI RVMPKKEGVI IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLK					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLD SAAEIYPMVLN YLGKNPNSSNT EDIREATALL KKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLD SAAEIYPMVLN YLGKNPNSSNT EDIREATALL KKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARDLMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

370

1315

m917.pep      ALKFMVRQWQDVKAGKX  
 |||||  
 g917          ALKFMVRQWQDVKAGKX  
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq  
 1    ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACAG  
 51   GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA  
 101   ACCGAAACGT ATTGAAAATT TACAACGGT CGGAATACGT CGATCCGGAA  
 151   ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT  
 201   GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCTG  
 251   GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAAG  
 301   GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA  
 351   CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG  
 401   AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC  
 451   GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCATG  
 501   GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA  
 551   TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACATAT  
 601   TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC  
 651   CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCTG  
 701   GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC  
 751   GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CCGGCGGCAA  
 801   GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG  
 851   ATTCTTTCGT GATTCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA  
 901   TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT  
 951   CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG  
 1001   AATTTAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTGAAAAAC  
 1051   AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG  
 1101   CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep  
 1    MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE  
 51   TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK  
 101   AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT  
 151   ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLSA AEIYPMVLNY  
 201   LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF  
 251   GGDNLNIAKRR AEEAGGKEKI RVMPKEGVG IWDVSFVIPK DAKNVANAHK  
 301   YINDFLDPEV SAKNGNFVY APSSKPAREL MEDEFKNDNT IFPTEEDLKN  
 351   SFIMVPIQPA ALKFMVRQWQ DVKAGK\*

m917/a917      99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m917.pep	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m917.pep	QCGISYLSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					

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a917      QCGISYLDAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      RGDTCVTIGFGGDLNIAKRRRAEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVITYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           ||||||||||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTCACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtagcgt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGGA AAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCACATC ACCGCGCGCA CAACGgcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCTT CCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGcgcTT GACGGCAAag cccCCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCAATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCGc tcgggcaaat acatCCGCAt cggATacgcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGetaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcatc aaagcCTATA TGCGGC AAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCCG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRSAL YGIAAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPYI GIPDDFISVP LPAGLRGGKN LVRIROTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGALG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```



This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

1	<u>MKKYLFRAL</u>	<u>YGIAAAILAA</u>	CQSKSIQTFP	QPDTSVINGP	DRPVGIPDPA
51	GTTVGGGGA	YTVVPHLSLP	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAFQTPVH	SFQAQFISFV	YFTPWQVAGN	GSLAGVTGTG	YEPVLKGGDR
151	RTAQAARFPI	GIPDDFISFR	LPAGLRSGKA	LVRIRQTGKN	SGTIDNTGGR
201	HTADLSRFPI	TARTTAIKGR	FEGSRFLPYH	TRNQINGGAL	DGKAPILGYA
251	EDPVELFFMH	IQGSGRLKTP	SGKYIRIGYA	DKNEHPVLSI	GRYMADKGYL
301	KLGGTSMQGI	KSYMRQNPQR	LAELVLQGNPS	YIFFRELAGS	SNDGPVGALG
351	TPLMGEYAGA	VDRHYITLGA	PLFVATAHPV	TRKALNRLIM	AQDTGSAIKG
401	AVRVDFYWG	DEAGEALAGK	OKTTGYVWQL	LPNGMKPEYR	P*

Homology with a predicted ORF from *N.gonorrhoeae*

m919/q919

	10	20	30	40	50	60
m919.pep	MKKYLFR	AALYGIA	AAAILAAC	QSKSIQ	TFPQPD	TSVINGP
	DRPVGIP	DPAGTT	VGGGGAV			
g919	MKKHLLR	SALYGIA	AAAILAAC	QSRSIQ	TFPQPD	TSVINGP
	DRPAGIP	DPAGTT	VAGGGAV			
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHL	SLPHWAA	QDFAKSL	QSFR	LGCANL	KNRQGW
	QDVCAQ	AFQTPV	HSFQAK	QFFER		
g919	YTVVPHL	SMPHWAA	QDFAKSL	QSFR	LGCANL	KNRQGW
	QDVCAQ	AFQTPV	HSFQAK	RFFER		
	70	80	90	100	110	120

1318

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
	:					
g919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	:					
g919	LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
	:					
g919	KLGQTSMQGIKAYMRNPQRLAEVLGQNPSYIFFRELAGSGNEGVPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFYFWGYGDEAGELAGK					
	:					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCGG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGCCCG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG CGGGGCGGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCC CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACCC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTCAAAC CCCCGTCCAT TCGGTTTCA GAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACTC CGGTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCGCTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTGGGCGCGC CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAG

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1319

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1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1 MKKYLFRAAAL CGIAAAILAA CQSKSIQTFF QPDTSVINGP DRPVGIPDPA
     51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFR LGCAN LKNRQGWQDV
    101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
    151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
    201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
    251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
    301 KLGQTSMQGI KAYMQQNQR LAEVLQNP S YIFFREL TGS SNDGPVGALG
    351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
    401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
           10      20      30      40      50      60
m919.pep  MKKYLFRAAALYGIAAAILACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
           |||||
a919       MKKYLFRAAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
           10      20      30      40      50      60

           70      80      90     100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFR LGCANLKNRQGWQDVCAQAFQTPVHVSFQAKQFFER
           |||||
a919       YTVVPHLSLPHWAAQDFAKSLQSFR LGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
           70      80      90     100     110     120

           130     140     150     160     170     180
m919.pep  YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
           |||||
a919       YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
           130     140     150     160     170     180

           190     200     210     220     230     240
m919.pep  LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
           |||||
a919       LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
           190     200     210     220     230     240

           250     260     270     280     290     300
m919.pep  DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
           |||||
a919       DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
           250     260     270     280     290     300

           310     320     330     340     350     360
m919.pep  KLGQTSMQGIKSYMQRNPQRLAEVLQNP S YIFFREL AGSSNDGPVGALGTPLMGEYAGA
           |||||
a919       KLGQTSMQGIKAYMQQNQR LAEVLQNP S YIFFREL TGS SNDGPVGALGTPLMGEYAGA
           310     320     330     340     350     360

           370     380     390     400     410     420
m919.pep  VDRHYITLGAPLFVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK
           |||||
a919       VDRHYITLGAPLFVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK
           370     380     390     400     410     420

           430     440
m919.pep  QKTTGYVWQLLPNGMKPEYRPX
           |||||
a919       QKTTGYVWQLLPNGMKPEYRPX
           430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtggtt cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacgggtt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaaagtgg acatcatCCC
501 CTTGcgcmaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAttccc
551 CCGATcaaAG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attetCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGCACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFPDQSVC  
 251 QKQANYSTLT FQIGHSHH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920 . pep				PMQLVTEK	KGKEMNIQ	RGTYNYQYRSNRPVK
m920	GGEYLKADL	GYGEFPELE	PIAKDRLHIF	SKPMQLVTEK	KGKEMNIQ	RGTYNYQYRSNRPVK
	40	50	60	70	80	90
g920 . pep						
m920	DGSYLVTA	EYQPTFRSK	NKAGWKQAGI	KEMPDASYCE	QTRMFGKN	IVNVGHESADTAIIT
	40	50	60	70	80	90
g920 . pep						
m920	DGSYLVIA	EYQPTFWSK	KKAGWKQAGI	KEMPDASYCE	QTRMFGKN	IVNVGHESADTAIIT
	100	110	120	130	140	150
g920 . pep						
m920	KPVGQNLE	IVPLDNPADI	HVGXRFKVR	VLFRGEPLNP	ATVTATFDG	FDTSDRSKTHKTEA
	160	170	180	190	200	210
g920 . pep						
m920	KPVGQNLE	IVPLDNPANI	HVGERFKVR	VLFRGEPLNP	ATVTATFDG	FDTSDRSKTHXXEA
	160	170	180	190	200	210
g920 . pep						
m920	QAFSDTTD	GEGEVDII	PLRQGFWKAS	VEYKADFPDQ	SLCRKQANYT	TTLTFQIAHSHHX
	160	170	180	190	200	
g920 . pep						
m920	QAFSDSTDD	KGEVDIIX	LQGFWKANVE	HKTDFPDQSV	CQKQANYSTLT	FQIGHSHHX
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920 . seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TGCGCGCATC
51	CGCCACGCC	CACCGCGTCT	GGGTGGAAC	CGCCACACG	CACGGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AAGGAAAAACA	TGATTCAACG	CGGCACATAC	AACTACCAGT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTTCTGGTC	AAAAACAAC	GCAGGCTGGA	AACAGGCGGG
351	CATCAAACAA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTTCG
401	GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCGCTGGCG
551	AACCGCTGCC	CAATGCCACC	GTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTTGCGC	CAAGGCTTCT
701	GGAAAGCCAA	TGTCGAACAC	AAAGCCGACT	TCCCCGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTTCGCA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920 . pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDLRHIFS	KPMQLVTEKG	KENMIQRGTY	NYQYRSNRPV	KDGSYLVIAE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHEADTAII
151	TKPVGQNLEI	VPLDNPANIH	VGERFKVRVL	FRGEPLNPAT	VTATFDGFD
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIPLR	QGFWKANVEH	KADFPDQSVC
251	QKQANYSTLT	FQIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVS	SALFATS	SAHAHRVW	VETAHTH	HGGEYLKADL	GYGEFPELEPIAKDRLHIFS
a920	XKKTLTLLAVS	ALFAASA	HAHRVW	VETAHTH	HGGEYLKADL	GYGEFPELEPIAKDRLHIFS
	70	80	90	100	110	120
m920.pep	KPMQLVTEKG	KENMIQR	GTNYQY	RSNRPV	KDGSYL	VIAEYQPTFWSKXKAGWKQAGIKE
a920	KPMQLVTEKG	KENMIQR	GTNYQY	RSNRPV	KDGSYL	VIAEYQPTFWSKNKAGWKQAGIKQ
	130	140	150	160	170	180
m920.pep	MPDASYCEQ	TRMFGK	NIVNVG	HESADTA	IITKPV	GQNLEIVPLDNPANIHVGERFKVRVL
a920	MPDASYCEQ	TRMFGK	NIVNVG	HESADTA	IITKPV	GQNLEIVPLDNPANIHVGERFKVRVL
	190	200	210	220	230	240
m920.pep	FRGEPLPN	ATVTAT	FDGFD	TSRDK	THXKEA	QAFSDSTDDKGEVDIIXLRQGFWKANVEH
a920	FRGEPLPN	ATVTAT	FDGFD	TSRDK	THKTEA	QAFSDSTDDKGEVDIIPLRQGFWKANVEH
	250	260	269			
m920.pep	KTDFPDQ	SVCQKQ	ANYSTLT	TFQIGH	SHHX	
a920	KADFPDQ	SVCQKQ	ANYSTLT	TFQIGH	SHHX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA  CATTGACACT  GCTCGCcggt  TcCGCACTAT  TTGCCACATc
51  cgCaCACCCC  CACCgCGTCT  GGGTCGAAAC  CgcccCACAg  cAegGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTCCCCGA  ACTCGAACCC
151 ATCGccAAAG  ACCgccTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGT  AAGGAAAAAC  TGATTCAACG  CGGCACATAC  AACTACCAAT
251 ACCGCAGCAA  CCGTCCCGTC  AAAGACGGCA  GCTACCTCGT  TACCGCCGAA
301 TATCAGCCTA  CTTCCCGTTC  AAAAAACAAA  GCAGGCTGGA  AACAGGCTGG
351 CATCAAGAA  ATGCCTGACG  CAAGCTATTG  CGAACAAACC  CGTATGTTCT
401 GTAAAAACAT  TGTCAACGTG  GGACACGAAA  GCGCGGACAC  CGCCATCATC
451 ACCAAACCGG  TCGGACAAAA  CTTGGAATC  GTCCCGCTGG  ACAATCCCGC
501 CAACATTCA  GTAGGCGAAG  GCTTCAAAGT  CCGCGTTCTG  TTCCGTGGCG
551 AACCGCTGCC  CAATGCCACC  GTTACCGCTA  CATTTGACGG  CTTCGACACC
601 AGCGACCGCA  GCAAAACGCA  CAAAACCGAA  GCCCAAGCCT  TCTCCGACAC
651 CACCGACGGC  AAAGGCGAAG  TGGACATCAT  CCCCTTGC GC  CAAGGCTTTT
701 GGAAAGCGAG  TGTGGAATAC  AAAGCCGATT  TCCCCGATCA  AAGCCTGTGC
751 CAAAAACAGG  CGAACTACAC  AACTTTAACC  TTCCAAATCG  GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV  SALFATS  AHP  HRVWVETAHT  HGGEYLKADL  GYGEFPELEP
51  IAKDRLHIFS  KPMQLVTEKG  KENMIQRGTY  NYQYRSNRPV  KDGSYLVTAE
101 YQPTFRSKNK  AGWKQAGIKE  MPDASYCEQT  RMFGKNIVNV  GHESADTAII
151 TKPVGQNLEI  VPLDNPANIH  VGERFKVRVL  FRGEPLPNAT  VTATFDGFD
201 SDRSKTHKTE  AQAFSDTTDG  KGEVDIIPLR  QGFWKASVEY  KADFPDQSLC
251 KQQANYTTLT  FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA  CATTGACACT  GCTCGCCGTT  TCCGCCCTAT  TTGCCACATC
51  CGCCACGCC  CACCGCGTCT  GGGTCGAAAC  CGCCACACG  CACGGCGGCG
101 AATACCTTAA  AGCCGACTTG  GGCTACGGCG  AATTTCCCGA  ACTCGAACCC
151 ATCGCCAAAG  ACCGCCTGCA  CATCTTCAGC  AAACCGATGC  AGCTGGTTAC
201 CGAAAAAGGC  AAGGAAAAAC  TGATTCAACG  CGGCACATAC  AACTACCACT
251 ACCGAAGCAA  CCGTCCCGTT  AAGGACGGCA  GTTACCTCGT  CATCGCCGAA

```

1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GTCATTCGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

```

m920-1.pep
1  MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFPDQSVC
251 QKQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1						
	10	20	30	40	50	60
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1						
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1						
	70	80	90	100	110	120
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL					
g920-1						
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL					
g920-1						
	130	140	150	160	170	180
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1						
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1						
	190	200	210	220	230	240
m920-1.pep	KTDFPDQSVCQKQANYSTLTFQIGHSHHX					
g920-1						
	250	260	269			
m920-1.pep	KTDFPDQSVCQKQANYSTLTFQIGHSHHX					
g920-1						
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

```

a920.seq
1  TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51  CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAATCG GCCATTTCGCA
801 CCATTAA

```

1324

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

a920.pep  
 1 \*KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFFPELEP  
 51 IAKDRLHIFS KPMQLVTEKG KENMIQRTY NYQYRSNRPV KDGSYLVIAE  
 101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII  
 151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD  
 201 SDRSKTHKTE AQAFSDSTD KGEVDIPLR QGFWKANVEH KADFPDQSV  
 251 QKQANYSTLT FQIGHSHH\*

m920-1/a920 98.9% identity in 267 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLLTLLAVSALFATS	SAHAHRVWVETAHTHGGEYLKADL	GYGEFFPELEPIAKDRLHIFS			
a920	KKKTLLTLLAVSALFAASA	HAHRVWVETAHTHGGEYLKADL	GYGEFFPELEPIAKDRLHIFS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m920-1.pep	KPMQLVTEKGKENMIQRTY	NYQYRSNRPVKDGSYLVIAE	YQPTFWSKNKAGWKQAGIKE			
a920	KPMQLVTEKGKENMIQRTY	NYQYRSNRPVKDGSYLVIAE	YQPTFWSKNKAGWKQAGIKQ			
	70	80	90	100	110	120
	130	140	150	160	170	180
m920-1.pep	MPDASYCEQTRMFGKNIVNV	GHESADTAITKPVGQNL	EIVPLDNPANIHVGERFKVRVL			
a920	MPDASYCEQTRMFGKNIVNV	GHESADTAITKPVGQNL	EIVPLDNPANIHVGERFKVRVL			
	130	140	150	160	170	180
	190	200	210	220	230	240
m920-1.pep	FRGEPLPNATVTATFDGFD	TSDRSKTHKTEAQAFSDSTD	KGEVDIPLRQGFWKANVEH			
a920	FRGEPLPNATVTATFDGFD	TSDRSKTHKTEAQAFSDSTD	KGEVDIPLRQGFWKANVEH			
	190	200	210	220	230	240
	250	260	269			
m920-1.pep	KTDFPDQSVCKQKQANYSTLT	FQIGHSHH				
a920	KADFPDQSVCKQKQANYSTLT	FQIGHSHH				
	250	260				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

g921.seq  
 1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG  
 51 Ccagtctatt tatGtgccca cattgacggA aatccccgTg aatccccatca  
 101 ataCCgtcaa aacggaagCA CTGCAAAAG GTTTTCGCCT CGCCCCCTCG  
 151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA  
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA  
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG  
 301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA  
 351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC  
 401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC  
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

g921.pep  
 1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFR LAPS  
 51 HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM  
 101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN  
 151 FLMEVMMKMP LK\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

m921.seq  
 1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG  
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA  
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCTCTTCG  
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA  
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA



1325

251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG  
 301 TATGAAATCT ACCTGCGTTC GCGATAGAC AGCCAGCGGG GCGCAATCAA  
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC  
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC  
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS  
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM  
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN  
 151 FLMEVMKMQP LK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	:					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAAT ACCTTATCCC TCTTTCATT GTGGCAGTTC TTTCCGGCTG  
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA  
 101 ATACGCTCAA AACGGAAGCA CCTGCAAAAG GTTCCGCCT TGCCTCTTCG  
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA  
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA  
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG  
 301 TATGAAATCT ACCTGCGTTC GCGATAGAC AGCCAGCGGG GCGCAATCAA  
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC  
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC  
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS  
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM  
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN  
 151 FLMEVMKMQP LK\*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1   ATGGAAGAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGCG GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTTGTG GACGATGAAG TCGGGAAAGG GGATTTTCC CAGGCGGAAT
251 GGCAGGATTT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATt
301 ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtggttcc gCacggGAAa
351 ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401 gcgcggttat cgatgatgtg gcgCAAAAt acggcgtGCC TGCCGAGCTT
451 ATCTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751 gcatcggTTG CCAATTAtat gaagCAGCAC GGTGGCGCA Cgggcggtaa
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATTT GAaggCGTAc
901 ggcacatccc ccggggaaaC GCTCGCAGAT GATGAAAAGg cgGTTTGTGTT
951 CAAACTGGAA ACCGCACCCG GCGTGTGTTGA ATATTATTTG GGCTTGAACA
1001 ATTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAAcGgcg
1051 gtcaggGACA TTGCCAATTC GCTCGGCGGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1   MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVGKGDFS QAEWQDFFDK AAYKADIVKI
101 MHRPSTSRPW YVFRGTNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFQK ELVELLKLAK
201 BEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGEKTAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMYVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1   ATGAAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGCG GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAAATT CGGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCTCG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG CCGGGGTTTT TCCAAAAAGA ATTGGTCGAG

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

1	MKKRKILPLA	ICLAALSACT	AMEARPPRAN	EAQAPRAVEM	KKESRPAFDA
51	AAVFDAAAVP	VSDSGFAANA	NVRRFVDDEV	GKGDFSRAEW	QDFFDKAAAYK
101	ADIVKIMHRP	STSRPWYVFR	TGNSGKAKFR	GARRFYAENR	ALIDDDVAQKY
151	GVPÆLIVAV	IGIETNYGKN	TGSFRVADAL	ATLGFDYPPR	AGFFQKELVE
201	LLKLAKKEEGG	DVFAFKGSYA	GAMGMPQFMP	SSYRKWAVDY	DGDGHRDIWG
251	NVGDVAAASV	NYMKQHGWRT	GGKMLVSATL	APGADVQAI I	GEKTALTRTV
301	ADLKAYGIIP	GEELLADEKA	VLFKLETAPG	VFEYYLGLNN	FYTWNQYNHS
351	RMVYTAVRDI	ANSLGGPGL*			

Homology with a predicted ORF from *N.gonorrhoeae*

m922/g922

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
	:					
g922	MEKRKILPLAICLAALSACTAMEARTPRANEQAQAPRADEMKKESRPAFDAA-----AVP					
	10	20	30	40	50	
	70	80	90	100	110	120
m922.pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
			:			
g922	VSDSGFAANANVRRFVDDEVGKGDFSQAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL					
	:    :	:	:	:	:	
g922	TGNSGRAKFHGARRFYAENRAVIDDVAQKYGVPAELIVAIIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m922.pep	ATLGFDDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFDDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
	250	260	270	280	290	300
m922.pep	DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKTALTRTV					
g922	DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKTALTRTV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m922.pep	ADLKAYGIIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIIPGETLADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					

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	300	310	320	330	340	350
		370				
m922 . pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922 . seq
1  ATGAAAAACA  GAAAAATACT  GCCGCTGGCA  ATTTGTTTGG  CGGCTTTGTC
51  TGCCTGTACG  GCGATGGAGG  CACGCCCGCC  CCGGGCAAAT  GAAGCCCAAG
101 CCCCCCGCGC  GGATGAAATG  AAAAAAGAAA  GCCGCCCGCG  GTTTGACGCG
151 GCAGCCGTAT  TTGACGCGGC  AGCCGTACCG  GTATCCGACA  GCGGGTTTGC
201 CGCCAATGCA  AATGTCCGCC  GTTTTGTGGA  CGATGAAGTC  GGGAAAGGGG
251 ATTTTTCCTG  GCGGAATGG  CAGGATTTT  TTGACAAAGC  GGCTTACAAG
301 GCGGACATCG  TCAAGATTAT  GCACCGCCCC  TCCACATCGC  GTCCGTGGTA
351 TGTGTTCCGC  ACGGGAAAT  CCGGCAAGGC  GAAATTTTCG  GGCGCGCGCC
401 GGTTTTATGC  GGAACCCGC  GCGCTTATCG  ATGATGTGGC  GCAAAAATAC
451 GGCGTGCCTG  CCGAACTTAT  CGTGGCGGTT  ATCGGGATTG  AAACGAATTA
501 CGGCAAAAAT  ACGGGCAGTT  TCCGTGTGGC  GGACGCATTG  GCGACCTTAG
551 GCTTTGATTA  CCCCCGCCGC  GCCGGGTTTT  TCCAAAAGA  ATTGGTCGAG
601 CTTTAAAGC  TGGCAAAAGA  AGAAGCGGCG  GATGTTTTTC  CCTTTAAAGG
651 CAGCTATGCG  GCGCAATGG  GGATGCCGCA  ATTTATGCCT  TCGAGCTACC
701 GGAAATGGGC  GGTGGATTAT  GACGGGGACG  GACATCGGGA  CATATGGGGC
751 AATGTTGGCG  ATGTCGCGGC  ATCGATTGCC  AATTATATGA  AGCAGCACGG
801 TTGGCGCACG  GCGGGGAAAA  TACTGGTGTC  TGCAACATTG  GCGCCGGGTG
851 CGGATGTTCA  GGCAATCATT  GCGGAAAAAA  CCGCCCTGAC  GCGGACGGTG
901 GCGGATTGTA  AGGCGTACGG  CATCATCCCC  GGCGAAGAGC  TTGCCGATGA
951 TGAAAAGGCG  GTTTTGTTC  AACTGGAAAC  CGCACCCGCG  GTGTTTGAAT
1001 ATTATTTGGG  CTTGAACAAT  TTTTATACGG  TATGGCAGTA  CAATCACAGT
1051 CGGATGTATG  TAACGGCGGT  CAGGGACATT  GCCAATTCGC  TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922 . pep
1  MKNRKILPLA  ICLAALSACT  AMEARPPRAN  EAQAPRADEM  KKEsrpafda
51  AAVFDAAAVP  VSDSGFAANA  NVRRFVDDEV  GKGDfSRAEW  QDFFDKAAYK
101 ADIVKIMHRP  STSRPwyvfr  TGNSGKAKFR  GARRfYAENR  ALIDDVAQKY
151 GVPaelivav  IGIETNYGKN  TGSFRVADAL  ATLGFDYPRR  AGFFQKELVE
201 LLKLAKKEEG  DVFAFKGSYA  GAMGMPQFMP  SSYRKWAVDY  DGDGHRDIWG
251 NVGDVAASIA  NYMKQHGWRT  GgKILVSATL  APGADVQAI  GEKtALTRTV
301 ADLKAYGIIP  GEELADDEKA  VLFKLETAPG  VFEYyLGLNN  FYTVWQYNHS
351 RMYVTAVRDI  ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922 . pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKEsrpafdaAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKKEsrpafdaAAVFDAAAVP					
	10	20	30	40	50	60
m922 . pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPwyvfr					
a922	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPwyvfr					
	70	80	90	100	110	120
m922 . pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPwyvfr					
a922	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPwyvfr					
	70	80	90	100	110	120
m922 . pep	TGNSGKAKFRGARRfYAENRALIDDVAQKYGVPaelivavIGIETNYGKNtGSFRVADAL					
a922	TGNSGKAKFRGARRfYAENRALIDDVAQKYGVPaelivavIGIETNYGKNtGSFRVADAL					
	130	140	150	160	170	180
m922 . pep	TGNSGKAKFRGARRfYAENRALIDDVAQKYGVPaelivavIGIETNYGKNtGSFRVADAL					
a922	TGNSGKAKFRGARRfYAENRALIDDVAQKYGVPaelivavIGIETNYGKNtGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep    ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922        ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
             190      200      210      220      230      240

             250      260      270      280      290      300
m922.pep    DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922        DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV
             250      260      270      280      290      300

             310      320      330      340      350      360
m922.pep    ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922        ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
             310      320      330      340      350      360

             370
m922.pep    ANSLGGPGLX
             |||||||||
a922        ANSLGGPGLX
             370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1   ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTCTGTGC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGCGG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GGCGCATACT TGGGTAGTAG GATGTTTCAAG CATAAAACGG
251 CGAAAAAGCG TTTTGTGTGT CTGTTCCGTC TGAAGTTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTT GTTCCGCCCG AACTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1   MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV V LFRLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1   ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTGTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GGCAGCATATT TCGGCAGCAT GACATTCAA CATAAGACAG
251 CGAAAAAGCG TTTTGTGTGT CTGTTCCGTC TGAAGTTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTGCGCT
401 TGTCTGATT TTTGTTAATC CACTATAT. T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1   MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRIPRHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV V LFRLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HXYFVPPF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923 .pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923 .pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFFVLFRLTVSGNVLATCILID-----					
m923	LLPALGGWVGAYFGSMTFKHKTAKKRFFVLFRLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923 .pep	-----YFVPPELFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923 .seq	1	ATGAAGCGGC	AGGCTTTCTT	CAAACTGATG	GCGTGTGCGG	CATTTCTGTC
	51	TGCCGTTTCG	CTGCGCCTCC	CCGTATTGGG	CGCGTGTTAC	GCAATATTGT
	101	CCCTCTATGC	GTTTGCACTT	TACGGCATCG	ACAAACGGCG	TGCCGTGCGG
	151	GGAAAACGCC	GCATTCCCGA	ACACCGCCTG	CTGCTGCCTG	CCTTGTTCGG
	201	CGGTTGGGCG	GGCGCATACT	TGGGCAGCAG	GATATTCAGG	CATAAAACGG
	251	CGAAAAAGCG	TTTTGTTGTG	CTGTTCCGTC	TGACTGTTTC	GGGCAATGTC
	301	CTGGCGACCC	TCATCCTGAT	TTATAGTGGA	TTAAATTTAA	ACCAGTACGG
	351	CGTTGCCTCG	CCTTA.GCTC	AAAGAGAACG	ATTCTCTAAG	GTGCTGAAGC
	401	ACCAAGTGAA	TCGGTTCCGT	ACTATTTGTA	CTGTCTGCGG	CTTCGTCGCC
	451	TTGTCCTGAT	TTTTGTTAAT	CCACTAT.AT	TATTTTGTCC	CGCCTGAATT
	501	TTTCGTAAAA	CTCGGCAGA	ATACCTGA		

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923 .pep	1	MKRQAFFKLM	ACAAFLSAVS	LRLPVLGACY	AILSLEYAFAL	YGIDKRRRAVR
	51	GKRRRIPEHRL	LLPALFGGWA	GAYLGSRIFR	HKTAKKRFFV	LFRLTVSGNV
	101	LATLILIIYS	GNLNQYGVAS	PXAQRERFSK	VLKHQVNRFR	TICTVCGFVA
	151	LS*FLLIHYX	YFVPPEFFVK	LGQNT*		

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923 .pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923 .pep	LLPALGGWVGAYFGSMTFKHKTAKKRFFVLFRLTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFFVLFRLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923 .pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFRITICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1   ATGAAACAAA TGCTTTTGGC cgtcggcggtg ggcgcggtgt TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgagggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1   MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVTGKKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQTA QAYLDARNAL PSNOTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1   ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTAATTCCTT

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1   MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAAMKDKIIAHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1   ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51 KINVFTGKEE SLLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKCKGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

## m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTTCA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAG
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

## m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGYFLN
51 NKIHVVTKGE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKCKGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGYFLNKHVVTKGE					
	:       :       :       :       :       :       :       :       :					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYFLNKHVVTKGE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKCKGQT					
	:       :       :       :       :       :       :       :       :					
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKCKGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX					
	:       :       :       :       :       :       :       :       :					
g925-1	AQAYLDARNALPSNQTYQQRQAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

## a925-1.seq

```

1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51 AAAAGACGGC GCGCTTTTCA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAG
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

## a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAAAMKDKI IAHQKCKGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

	10	20	30
a925-1.pep	NKINVFTGKEESMLLSEKDGALSINTGIGE		
	:       :       :       :       :       :       :       :		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGYFLNKHVVTKGEESLLLSEKDGALSINTGIGE		
	30	40	50
	60	70	80
	40	50	60
	70	80	90



1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1      IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
                      90      100      110      120      130      140

a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
                      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAactGC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GGCGGGCGCG CCTtaccGCA
401 TCCGTTcAGA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAactGC CAATCCAATA
351 TCTGCATATC TGGGCGAGAT GCAGGCGTGT GGCGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAAC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCAGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGR
151 ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

g926.pep      10      20      30      40      50      60
MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926          10      20      30      40      50      60
MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ

g926.pep      70      80      90      100     110     120
PPVETININTPLGSTLGQLCQDRDGALAVDGGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
|||||
m926          70      80      90      100     110     120
PPVETININTPLGSTLGQLCQDRDGALAVDGGKGNVYQAESEELSRQLVGFKLPIQYLHI

g926.pep      130     140     150     160
WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCRQWGASPNVATE

```

1334

m926      ||:|||||      |||||      ||:|      :|  
WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS  
                 130            140            150            160            170            180

## a926.seq

```

1   ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGC GC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAAC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATT
501 GAACATCAGG CTGGTTTTC CCGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCAAGAACA ATGCGCGGCA CGCATACAGT AA

```

## a926.pep

```

1   MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEKGK
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGLAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADSGGQVRTL QLNNGNLNI RLVFTEIGMPS ETETQEQA RIQ*

```

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPS EHISSFAEGR LAVKAEKGKSYANFDWTYQ					
	:             :             :             :             :					
a926	MKHTVSASVILLTACAQLPQNNENLWQPS EHTRSFTAEGRLAVKAEKGKSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGLAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGLAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
	:					
a926	ETETQEQAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

## g927.seq

```

1   atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51  CAGCCCcgca GCcgatTcaa accaTCCGTC CGGAcAaAAT GCCCCGGCCA
101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

```

1335

```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATAACGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAAGCTCGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

```

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VTRYFYKEYD HLFVGTQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
201 LKNTVPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

```

1 ATGAAACCTT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
51 CAGCCCCGCA GCGGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGCCA
101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCACGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAACCTCG GGCAACGGAC GCTACGCTT CCTCGGCGCA TACGGTTACG
551 GTCTGAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GcKcGcCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTTGAAAA
701 CGAAGCCAAC TACGTCAGCt AAAAActGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

```

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYLKTNTG NEQEAQKLVA
201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
g927.pep	HLFVGTQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
m927	PLFIKTYQSEHPGTSVSIQQSHGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNRYAFLGA					
	130	140	150	160	170	180

1336

```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTVPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTS
          |||||:|||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          ||||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GTCACGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTGA AAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAA ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGSSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NNGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:|||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGSSSKQALSVANGLQADVVTMNQSSDIDLEKKGLVEK
          |||||:|||||
a927      PLFIKTYQSEHPGTSVSIQQSHGSSSKQALSVANGLQADVVTMNQSSDIDLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:|||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTSA
          |||||:|||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```

1337

m927.ppep KNX  
 111  
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq  
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG  
 51 CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT  
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG  
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT  
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GCGGATGAGC GATGCGTTGA  
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT  
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT  
 351 TATCGCCGTT TTTGGAAGAA AAACgctggg CATCGGTTAC AGTCTCGCTC  
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC  
 451 GGCGGCATTA TACATCcgat TATGCagtcg attgCcggCA GttacggctC  
 501 caatCCCACA AAAGGCACag aaggcaagat gggtAAATAT TtggcTTtgg  
 551 tcaattaTCA TTCcaatCCC atttcgctcg ctAtggctat taCTGcaact  
 601 gCCCCcaacc CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag  
 651 tttccgtCTT Tcttgggggg cgTGGGcgtg ggcaaTGGCT Gttccccggc  
 701 ttatcgccct TtctgTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT  
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGTCGAG  
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG  
 851 GTATTCTGCT GCTGTTGTGG GCAGATGTC CCGCCCTTAT TACCGGCAAT  
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT  
 951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA  
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA  
 1051 TTTTtaAATA Aactcggact gattaaatGG TTCTCCGGAG TGTGGCGGA  
 1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG  
 1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT  
 1201 ATTACCGCTA TGTCGGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC  
 1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA  
 1301 TGACCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG  
 1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTTA TCATGAGCGT  
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGG TGGAAAGTTC  
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.ppep  
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK  
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI  
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG  
 151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMAITAT  
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP  
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN  
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA  
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMPASTTAH  
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS  
 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq  
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG  
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT  
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG  
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT  
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GCGGATGAGC GATGCGTTGA  
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT  
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT  
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC  
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

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```

451  GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501  CAATCCC CGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551  TCAACTATCA TTCCAATCCC ATTTTCGTCGG CTATGTTTAT TACTGCAACT
601  GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651  TTCCGCTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701  TTATCGCCTT TTTCTGTTATG CCTTTGATTT TATATTTwyT GTATCCGCCT
751  GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801  GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851  GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901  CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951  GCTTTTGCTT TCCGGTGTAT TGA CTGTTGGG CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTCGGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTTCGGTTCG
1351 GGTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

```

m929.pep
1  MKLGFKPIPL AIAAVLCALV LALVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng)

from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALVPDGVK PQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929.pep	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929.pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
g929.pep	LALVNYHNSP ISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929.seq
1  ATGAAATTGG  GTTTCAAACC  GATACCCCTC  GCCATTGCCG  CAGTATTGTT
51  CGCCTTGGTT  TTGGCACTGC  CCGTACCCGA  CGGGGTCAAG  CCTCAGGCTT
101  GGACGCTGCT  GGCCATGTTT  ATCGGTGTGA  TTGCCGCCAT  TATCGGCAAG
151  GCCATGCCGT  TGGGTGCGCT  GTCGATTATT  GCCGTGCGGT  TGGTCGCAGT
201  AACCGGCGTA  ACCGCCGACA  AACCGGTGTC  GGCGATGAGC  GATGCGTTGA
251  GTGCGTTGCG  CAATCCGTTG  ATTTGGCTGA  TTGCCATCGC  AGTTATGATT
301  TCGCGCGGTT  TGCTCAAAAC  AGGGCTGGGG  ATGCGTATCG  GATATTTGTT
351  TATCGCCGTT  TTTGGAAGAA  AAACGCTGGG  CATCGGTTAC  AGTCTCGCTC
401  TTTCCGAACT  GCTGCTGGCT  CCCGTTACCC  CTTCCAATAC  CGCGCGCGGC
451  GCGGCGATTA  TACATCCGAT  TATGCAGTCG  ATTGCCGGCA  GTTACGGCTC
501  CAATCCCGCA  AAAGGCACAG  AAGGCAAGAT  GGGTAAATAT  TTGGCTTTGG
551  TCAACTATCA  TTCCAATCCC  ATTTGCTCGG  CTATGTTTAT  TACTGCAACT
601  GCCCCCAACC  CTTTAATCGT  CAACTTGATT  GCCGAAAATT  TAGGCAGTAG
651  TTTCCGTCTT  TCTTGGGGGG  CGTGGGCGTG  GGCAATGGCT  GTTCCCGGCG
701  TTATCGCCTT  TTTCGTTATG  CCTTTGATTT  TATATTTTTT  GTATCCCGCT
751  GAAATTAAAG  AAACGCCCAA  TGCCGTTCAA  TTTGCCAAAG  ACCGTCTGAG
801  GGAGATGGGT  AAAATGTGCG  CAGACGAAAT  CATTATGGCG  GTCATTTTCG
851  GTATCTTGTT  GCTGTTGTGG  GCAGATGTTT  CCGCCCTTAT  TACCGGCAAT
901  CACGCTTTTA  GTATCAACGC  CACCGCCACC  GCATTTATCG  GATTAAGCCT
951  GCTTTTGCTT  TCCGGTGTAT  TGACTTGGGA  CGATGTTTTG  AAAGAAAAAA
1001  GCGCGTGGGA  TACGATTATT  TGGTTTGGCG  CATTGATTAT  GATGGCCGCA
1051  TTTTAAATA  AACTCGGACT  GATTAAATGG  TTCTCCGGAG  TGTGGCGGGA
1101  AAGTGTCGGC  GGTTCGGGCG  TTAGCGGCAC  GGCTGCGGGC  GTAATCCTCG
1151  TGCTTGCTTA  TATGTATGCG  CATTATATGT  TTGCCAGTAC  TACTGCACAT
1201  ATTACCGCTA  TGTTCCGGCG  ATTTTTCGCT  GCTGCCGTTT  CACTGAATGC
1251  CCCGGCGATG  CCGACCGCGC  TGATGATGGC  GGCCGCATCT  AACATTATGA
1301  TGACCCTCAC  TCATTATGCG  ACCGGTACTT  CGCCTGTGAT  TTTCCGGTTCG
1351  GGCTACACCA  CAATGGGAGA  ATGGTGGAAG  GCGGGTTTAT  TCATGAGCGT
1401  AGTCAATTTT  CTGATTTTTT  TCGTTATCGG  CAGCATTGTT  TGGAAAGTTC
1451  TGGGGTATTG  GTAA

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1340

This corresponds to the amino acid sequence &lt;SEQ ID 2850; ORF 929.a&gt;:

```

a929.pep
  1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
 51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAMI
101  SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151  GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201  APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251  EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301  HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351  FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMEASTTAH
401  ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451  GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

	10	20	30	40	50	60
m929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGIVIAAIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGIVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAMI SRGLLKTGLG MRIGYLFIAV					
a929	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAMI SRGLLKTGLG MRIGYLFIAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m929.pep	FGRKTLGIGY SLALSELL LAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTLGIGY SLALSELL LAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m929.pep	LALVNYHNSP ISSAMFITAT APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM					
a929	LALVNYHNSP ISSAMFITAT APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m929.pep	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
a929	PLILYFLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m929.pep	HAFSINATATAF IGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA FLNKLGLIKW					
a929	HAFSINATATAF IGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA FLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
m929.pep	FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMEASTTAH ITAMFGAFFAAVSLNAPAM					
a929	FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMEASTTAH ITAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
m929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					



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a929 WKVLGYWX

g930.seq not found yet  
g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAC GAATGGGTGT TGGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201 ACGTATTGCA GCATTCCAAA ACAAAATTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCGCGTAACG TCTGTGCCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGA CTGAGTG ATATGTTCTA
501 TGTAATTTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701 GTTACAACAC TGATTTCCGG TCAACCGGCC TGTGTATATG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAAGTTA
801 CATTGATGAT GCCGAAC TGTACAACG GCGTAAAC ACAGGTTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGCGCGCGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CCGGTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGCGAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTTATCGGG CCAAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAAAC GGGTTTCAGG TGGGTTATTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKLCP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYSVSKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FGEGTSRMKI WTASADVNTF FQIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNHLHYD

```

451 IFTGRALKKP EYFQTKKWT GFQVGYSF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```
1 ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAC GAAGTGGTGT TGGAAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAAATCATG TCCTTAGCAC
401 AAATGCTTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGA TACCGAGCTA
501 TCTGCCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAAATTA TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCCTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAAACTGTG GATGAGGGAA ACAAAAAGTT
1151 ACATTGATGA TGCCGAACTG ACTGTACAAC GGCGTAAAC TGCGGGTTGG
1201 TTGGCAGAAC TTTCCACAAA AGAATATATC GGTCCGAGTA CGGCAGATT
1251 TAAGTTGAAA TATAACGCG GCACCGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTAC GTATGAAAAA TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAACAGC TATTTCCTTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACTGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTAAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTACAGACA ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA
1701 TATATTACC GGCCGCGCAT TGA AAAAGCC CGAATTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2856; ORF 930-1&gt;:

m930-1.pep

```
1 MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QODIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFO NKFPTSRNDL
201 LNLRLDLEQGL ENLKRLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDNSGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHRRKGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQAVSG LSEVVDYNGK
351 SYNTDFGFNR LLYRDAKRKT YLGVKLMWRE TKSYYIDDAEL TVQRKRTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTGMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTFFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWY WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*
```

m930-1/g930-1 95.4% identity in 478 aa overlap

```
90      100      110      120      130      140
m930-1.pep AINEVVLEGEHHRFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTTRI
g930-1.pep      |||||:|||||
                GKCLHAGDINQIMSLAQNALIGRGYTTTRI
                        10      20      30

150      160      170      180      190      200
m930-1.pep LAAPQDLNSGKLQTLTIPSYLRSIRIDRSNDDQTHAGRIAAFO NKFPTSRNDLLNLRDLE
g930-1.pep      |||||:|||||
                LAAPQDLNSGKLQTLMPGYLRSIRIDRSNDDQTHAGRIAAFO NKFPTSRNDLLNLRDLE
                        40      50      60      70      80      90

210      220      230      240      250      260
m930-1.pep QGLENLKRLPTAEADLQIVPVEGEPNQSDVVVQWRQRLPYRVSVGMDNSGSEATGKYQG
                ||||| ||||| ||||| ||||| ||||| |||||
```

1343

```

g930-1.pep  QGLENLKCCLPTAEADLQIVPVEREPNOSDVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150

              270      280      290      300      310      320
m930-1.pep  NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAFPGKWTWAF
              |||
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAFPGKWTWAF
              160      170      180      190      200      210

              330      340      350      360      370      380
m930-1.pep  NHNGYRYHQAVSGLSEVYDYGKSYNTDFGFNRLLYRDAKRKTYLGVKLWMRETKSYIDD
              |||
g930-1.pep  NHNGYRYHQAVSGLSEVYDYGKSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDD
              220      230      240      250      260      270

              390      400      410      420      430      440
m930-1.pep  AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTGMKDALARPEEAFGEGTSRMKI
              |||
g930-1.pep  AELTVQRRKTTGWLAELSHKGYIGRSTADFKLKYKHGTGMKDALARPEEAFGEGTSRMKI
              280      290      300      310      320      330

              450      460      470      480      490      500
m930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
              |||
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390

              510      520      530      540      550      560
m930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              |||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450

              570      580      590
m930-1.pep  IFTGRALKKPEFFQSRKWASGFQVGYTF
              |||
g930-1.pep  IFTGRALKKPEYFQTKKWVTGFQVGYSEFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
  1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
 51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
101  ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAAC CGTTGCCAAT
151  TTCGTGCGCT ATGCCCCGAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201  CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251  TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301  AAAAAACCCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351  CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401  ACAAAAACGG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451  ATGGACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501  TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTTGTCG
551  GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCC TTTCCAAAAA
601  AACGCCGTTT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2858; ORF 931.ng&gt;:

```

g931.pep
  1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
 51  FVRYARKGFY DNTIFHRVIG GFVIQDGLT EDLVQKATDK AVANESGNGL
101  KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151  MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

1344

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

m931.seq

```

1  ATGAAACCCA AATTCAAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GTTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTGCGCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACcA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

m931.pep..

```

1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPVKIRR					
	130	140	150	160	170	180
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

a931.seq

```

1  ATGAAACCCA AATTCAAAAC CGTTTAAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTGCGCA ACGAATCCGG CAACGGCTTG
301 AAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC

```

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451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT  
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTCCG  
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep  
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN  
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL  
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG  
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ\*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLT	ALLLAVSLPS	MAATHVLMET	DMGNIRLVLD	ESKAPKTVAN	FVRYARKGFY
a931	MKPKFKTVLT	ALLLAVSLPS	MAATHVLMET	DMGNIRLVLD	ESKAPKTVAN	FVRYARKGFY
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVID	GFVIQGGGLT	EDLAQKASDK	AVANESGNGL	KNTAGTIAMART	TAPDSATS
a931	DNTIFHRVIG	GFVIQGGGLT	EDLAQKASDK	AVANESGNGL	KNTVGTIAMART	ADPDSATS
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXX	SLDYKNGQYG	YTVFGRVESG	MNTVSKIARV	KTATRGFYQN	VPVQPVKIRR
a931	QFFINLVDND	SLNYKNGQYG	YTVFGRVESG	MNTVSKIARV	KTATRGFYQN	VPVQPVKIRR
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq  
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC  
 51 GTTTGGGGGA TTTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT  
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC  
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG  
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA  
 251 GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAAACAA  
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep  
 1 MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD  
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK  
 101 KYEWPREEGK TK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows \_\_\_% identity over a \_\_\_ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq  
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCACC GC

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```

51  CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTGAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCCCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GGCGCGTCAA TGCCGTCTGA AGGGCTTTCA GACGCATTTT
601 TTGTATTTGT TAGGGGCATT GTTATGTTGC CGTTTGATTT TCAGACGGCA
651 TTTTGTTC AAGCGTTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1  MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAQAQANGNN GQPVTGKRRR AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQRAG KQIHTGGQPR QPRRPSRACC LPSVRTPQCA HQQGFHAQAP
151 PCKTTGGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPAPQ CRLKGFQTA
201 LYLLGALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1  ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51  ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCC TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCCTGGTC GGCGCGGCGG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAAATTCAC ACGGCGCAGC AACCAAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
451 CCCCCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCGG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTnT GCATTTGTTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1  ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51  TGXRRAAVYL RPIDRKLAAA KPGRRGRRV YRQRAGKQIH TGRQPRQSR
101 PARACSLPSV RTPQAHQQG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFQEA VNPARQCRLK SFQAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

		10	20	30	
m934.pep		RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI			
		:			
g934	MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI				
	10 20 30 40 50 60				
	40 50 60 70 80 90				
m934.pep	PAEAQANGNNGQPVGTGXRRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR				
	:				
g934	PAQAQANGNNGQPVTKRRAAVYLRPIDRKLAAAKPDWRGRRVYRQRAGKQIHTGGQPR				
	70 80 90 100 110 120				
	100 110 120 130 140 150				

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```

m934.pep  QSRRLPARACSLPSVRTPQCAHQQGFHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
           |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g934      QPRRPSRACCLPSVRTPQCAHQQGFHAQPPCKTTGGAGAALPPDNAPARQLPPSRYARF
           130      140      150      160      170      180

           160      170      180      190      200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
           ||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g934      RQKAVNPARQCRLKGFQTAFLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
           190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2869>:

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCG
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TGCGCGGTTT CGGCAGAAGG
551 CGGTAAATCC GCGGTGCCAA TGCCGTCTGA AGGGCTTCA GACGGCATT
601 TTGTATTGTG TAGGGACATT GTTATGTTGC CGTTTGATTT TTAGACGGCA
651 TTTTGTTC AAGAGTTTGA TGTCGGGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2870; ORF 934.a>:

```

a934.pep
1  MKKIIASALI ATFALAACQD DAQARLEQQQ KQIEALQQQL AQQADDTVYQ
51  LTPEAVKDTI PAEAQANGNN GQPVTX*RRR AVYLRPIDRK LAAAKPGRRG
101 GRRVYRQAG KQIHTGRQPR QSRRLPARACR LPSVRTSQCA HQQGFHAQF
151 PCKTTGGAGA ALPPDNAPAR QLPPPRHARF RQKAVNPACQ CRLKGFQTAF
201 LYLGLTLLCC RLIFRRHFVS KSLMSGWQF*

```

m934/a934 94.1% identity in 205 aa overlap

```

           10      20      30
m934.pep  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
           10      20      30      40      50      60

           40      50      60      70      80      90
m934.pep  PAEAQANGNNGQPVTXRRRAVYLRPIDRKLAAAKPGRRGRRVYRQAGKQIHTGRQPR
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      PAEAQANGNNGQPVTXRRRAVYLRPIDRKLAAAKPGRRGRRVYRQAGKQIHTGRQPR
           70      80      90      100     110     120

           100     110     120     130     140     150
m934.pep  QSRRLPARACSLPSVRTPQCAHQQGFHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      QSRRLPARACRLPSVRTSQCAHQQGFHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
           130     140     150     160     170     180

           160     170     180     190     200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
           ||:||||| ||||| ||||| ||||| ||||| ||||| |||||
a934      RQKAVNPACQRLKGFQTAFLYLLGTLCCRLIFRRHFVSKSLMSGWQFX
           190     200     210     220     230

```

g935.seq not found yet

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAATC
801 AGCTTATGAC GACGGGTTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCCGCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAAA CCGGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTG CGGTTGTGC CGAAACGCGA AACGGTGGCG
1201 GCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGCTG
1251 GCGCGAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCGCGCT
1301 CTTATGCCCG CCGCAACTAT AAGGCGGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

a935.pep

```

1 MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGHGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPIYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGLVWVWCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
a935	MLYFRYGLVWVWCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300



g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCGCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAAGTGTCA GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCG GTAAAAAATC
801 AGCTTATGAT GACGGGTTTCG GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCACTCG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CCGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CCGTTTGTGC CGAAACCGGA AACGGTGGGC
1201 GCGCGCGTCA ATAATGCCGC CTACCGGCGC AACGGTGTGT ATGCCGGTTG
1251 GCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCC CCGCAACTAT AAGGGCATTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP ABAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEEAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLW QYKNAROTAG ILPFYQVQLS
301 GSDGFDATK RVNRRLLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAARR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFSV
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGAAGGCGCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAATT
501 GGATTTGCCG GCGCCGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CCGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFD	AKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE				
a935	GSDGFD	AKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE				
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEAOQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGIAAFSTEAOQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNV	PYAKRRNSEVFVSADWRF				
a935	GRTESNV	PYAKRRNSEVFVSADWRF				
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGCGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgcgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGC AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPPEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```

1351

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

	10	20	30	40	50	60
m936 . pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	:     :     :     :     :     :					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936 . pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	:     :     :     :     :     :					
g936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130					
m936 . pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936 . seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCCTCAG
51	CCTTGCCCTC	GGCGGCTGCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGTCG
101	GCGCGAAATC	CGCCGTCGAC	CGCCGAACCA	CCGGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCACC	GCCCGCTCCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTCGGTC	AGATTGCACG	TTCCGAACAG	GCCGCCGAAG	GCGTGTACAA
351	CTACATTACC	GTCGCCTCCC	TGCCGCGCAC	TGCCGGCGAC	ATCGCCGGCG
401	ACACTTGGA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTCACCCCGG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936 . pep

1	MKPKPHTVRT	LTAAVLSLAL	GGCVSAVVGG	AAVGAKSVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQNNQ	TKGYTPQISV	VGYNRHL	LLLGQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLPRTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	QR*				

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936 . pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT					
	:     :     :     :     :     :					
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAVGAKSVDRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936 . pep	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	:     :     :     :     :     :					
a936	ARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936 . pep	VASLPRTA					

a936
 

|||||  
 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT  
 130            140            150            160            170            180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1   ATGAAACCCA AACACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCaccgT CGCGGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1   MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVTITLYQNYV
201 QR*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1   ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGCGCGCA AACCAGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGCGCAC ATCGCCGGCG
401 ACACCTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1   MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVTITLYQNYV
201 QR*
  
```

m936-1/g936-1 95.5% identity in 202 aa overlap

	10	20	30	40	50	60
m936-1.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASVDRRTTGAQTDDNVMALRIETT					
	:     :     :     :     :     :					
g936-1	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAASVDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT					
	:     :     :     :     :     :					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLLLQGVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					
	:     :     :     :     :     :					

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCTCT GCGGCTGCGC TCAGCGCAGT CGTCGGCGGC GCGGCGGTCTG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCTG CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTAGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVSAVVG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GOVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAVGAASAVDRRTTGAQTDDNVMALRIETT
              ||::|||:|||||:|:|||||
a936-1      MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGVGAASAVDRRTTGAQTDDNVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLALLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLALLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTAgt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctga acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTcAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccga CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACCTCGacg GCAACGGCAA

```

q937.pep

1	MKNILLVFVS	FVPLCVRTL	PLNIEDIMTD	KGKWKLETSL	TYLNSNSRA
51	<u>ALASPVYIQT</u>	GSASFIPVPT	EIQENGSNTD	MLAGTLGLRY	GLTGNTDIYG
101	SGSYLWHEEL	KLDGNGKTRN	KRMSDISAGI	SHTFLKDGKN	PALIAFLEST
151	VYEKSRNKAS	SGKSWLIGAT	TYKAIDPIVL	SLTAAYRING	SKTSLSDVDKY
201	KAGNYWMLNP	NISFAANDRI	SLTGGIQWLQ	KQPDRIIDGKK	ESARNTSTYA
251	HFGAGGFGFTK	TAALNASARF	NVSGOSSSEL	KGLVOHTF*	

m937.seq

1	ATGAAGCGCA	TCTTTTGGCC	CGCCTTGCCC	GCCATCCTGC	CTTTATCCAC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
101	AATGGAAACT	GGAAACTTCC	CTTACCTACC	TGAACAGCGA	AAACAACCGC
151	GCCGAACCTG	CCGCACCGGT	TTACATTCAA	ACCGGCGCAA	CCTCGTTTAT
201	CCCCATTCCG	ACCGAAATCC	AaGAAAaCGG	CAGCAATAAC	GATATGCTCG
251	TCCGCACGCT	CGGTTTGGCG	TACGGACTGA	CCGGGAATAC	CGCATTTTAC
301	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACCTG	ACGGCAACAG
351	CAAAACCCGC	AACAAACGGA	TGTCCGACGT	ATCCCTCGGC	ATCAGCCACA
401	CTTTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAAGC
451	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTCCGGGA	AATCCTGGCT
501	CATCGGCGCC	ACCACCTACA	AAGCCATAGA	TCCGATTGAT	CTTTCCTCTA
551	CGCCCGCCTA	CCGCATCAAC	GAGCAGAAAA	CCCTTTCAGA	CGGCATCCGC
601	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACATCT	CATTTGCTGC
651	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATGGCTG	GGCAGGCAGC
701	CGACCCGGAC	GGACGGCAAA	CGGGAATCCT	CCAGAAACAC	ATCCACCTAC
751	GCCCATTTCG	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACGC
801	ATCCCGACGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCGGAA	CTGAAATTTG
851	CGGTACAGCA	TACATTTTAA			

m937.pep..

1	<u>MKRIFLPALF</u>	<u>AILPLSTYAD</u>	<u>LPLTIEDIMT</u>	DKGKWKLETS	LTYLNSENNR
51	<u>AELAAPVYIQ</u>	TGATSFPIPI	TEIQENGSN	DMLVGTLGLR	YGLTGNTDIY
101	GSGSYLWHEE	RKLDGNSKTR	NKRMSDVSLG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPIV	LSLTAAYRIN	GSKTSLSDGIR
201	YKSGNYLLLN	PNISFAANDR	ISLTGGIQLW	GRQPDRTDGG	RESSRNTSTY
251	AHFGAGYFGFT	KTTALNASAR	FNVSGQSSSE	LKFGVOHTP*	

Homology with a predicted ORF from *N.gonorrhoeae*

q937/m937

	10	20	30	40	50	59
g937.pep	MKNILL-VFVSFVPLCVRTLPLNIEDIMTDKGKWKLETSLTYLNSENRAALASPVYIQ					
	:  :: ::   : :   :     :     :     :     : :    :					
m937	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
g937.pep	60	70	80	90	100	119
	TGSASFIPVPTEIQENGSENTDMLAGTLGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR					

```
a937.seq
  1  ATGAAGCGCA TCTTTTGGCC GGCCTTGCCC GCCATCCTGC CTTTATCCGC
51  TTATGCCGAC TGCCCTTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GTGAACTTCC CTTACCTACC TGAACACGCA AAACACCCGC
151 GCGGAACCTT CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA ACAAACCGGA TGTCCGACGT ATCCTCGCGC ATCAGCCGCA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCGTCGTC CTCTCATTTA
551 CCGCTGCCTA CCGTATCAAC GCGAGCAAAA CCCTTTCAG CAACACCAAA
601 TACAAGCAG GCATTACTG GATGCTGAAT CCAATATAT CTCTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA
```

```
a937.ppe
  1 MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
  51 AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLGR YGLTGNTDIY
 101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
 151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSNNTK
 201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
 251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	:					
a937	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m937.pep	TGATSFIPPIPTETQENGSTNDMLVGTGLGLRYGLTGNTDIYSGGSYLWHEERKLDGNSKTR					
	:					
a937	TGATSFIPPIPTETQENGSTNDMLVGTGLGLRYGLTGNTDIYSGGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m937.pep	NKRMSDVSLSGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLSGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTD GK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLD GK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence &lt;SEQ ID 2894; ORF 939&gt;:

m939.pep (partial)

```

1  MKRLTLIAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHOTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CCGTGAAGCC AATCCTAAGG AAAATCCC GA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTGAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTCGGC
601 AACTTTATCC AAGGTTTGCG TTAA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2896; ORF 939.a&gt;:

a939.pep

```

1  MKRLTLIAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHOTIGIRD GKRTGSAAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPKENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVIEQ MNAYKSGQRK NTIMEDIANR MSEDLDKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.p	MKRLTLIAFVLAAGAVSASP KADVEKGKQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					
a939	MKRLTLIAFVLAAGAVSASP KADVEKGKQVAATVCAACHAADGNSGIAMY PRLAAQHTAY					



1357

```

                10      20      30      40      50      60
                70
m939.pep      IYHQTIGIRDVNAP
                |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDQDILNVSAFYAKQPKSGEANPKENPELGA
                70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGCGC GCCGTGTCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGC GCGC CATCCAAATC TGCCGAAGGT
151 TCGTGC GCGC CATCCAAATC TGCCGAAGGT TCGTGC GCGC CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAGGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGC GCGC CGTCCAAATC TGCCGAAGGT
151 TCGTGC GCGC CGGCTGCTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

                10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
                |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQGSAGGSCGASKSAEG
                10      20      30      40      50      60

                60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
                |:|||||
g950          SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
                70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGC GCGC CGTCCAAATC TGCCGAAGGT
151 TCGTGC GCGC CGGCTGCTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

1358

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKS AHG SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a950.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS	AHGS	CGASKSAEGSCGAAGSKAG			
m950	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS	AHGS	CGASKSAEGSCGAAGSKAG			
	10	20	30	40	50	60
	70	80	90	100		
a950.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m950	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCTACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTC ACCTGTGTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TGCGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTTGGAA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCC CCGTGCAGCG
601 TTGAAGTAGT AACATCTGCC CGAAGCGGCG GTTGCCGATG CCGTGTTCGG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTTAATGAC GTTGCCTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAATT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGA CTTGCTGTGTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTTGGCGG
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTCGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGTTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GGCAGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCCGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAATC AACCCGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCATT TGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGCAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGAATCG CTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GOAYAAGAAD VELPKEVGKV LRKHRRYSEE
```

1359

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHLDGLE EVLAQSDDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFEEQTDTON LSAVWQEMEI MNLVSLRKP DAYARLNVLL
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKVS APEYLFDKGV LAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLLGD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGGCGAGCG
201 GGTTAATCAG ATATTACGT TGCTGGGAGG GGAAACCGCC TTGCAAAAGG
251 GGCAGCGGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGCGGAAA TGATTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AACCGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAGG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGGACGAGG GGACAGAACC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTG GCGCAAAAG CATCGAAAGC GGTTCGCCCG
601 GCGGCGTTGA AATATGAACA TCTGCCCGAA GCGGCGGTG CCGATGTGGT
651 GTTCAGCGTA CAGGGACGCG AAAAGGAAAA GGCAATCGGA GCTTTGCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCGAAATA CTGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGCTCG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CTTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTG
901 CTGTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GCGCGCAACG CGAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGACG GAGGAACAGC GGAGCAGGCG GCGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAAGT
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CCGCTGCGCG GGCTGTGCGG TTGGACGGCG GCAGGGCGGC TTTGCGGCGC
1201 ATTCGCGAGG TGCGGAAACT TCCGAAACAG CAGGGGCGGT ATTTTACGCG
1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CCTGTGCAAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCTTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAAGTTG
1401 TTACGATCGG CTTGGCAAGC GGAATAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATA CAAATCAACC CCGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGCGCTA TTACCTGAAA GCGCAGCGCG AAAGCGCGCT GCCGTATCTG
1651 CCGTATTCTG TTGAAAACGA CCCCAGCGCC GAAGTTGCCG CCCATTGCGG
1701 CGAAGTGTGG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGCGCGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCCGAAAC CTCGGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRFKM LTVLTATLIA GQVSAAGGGA GDMKQPEVG KVFRKQQRYS
51 EEEIKNERAR LAAVGERVNO IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYEHLP EAAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLTKYPEI LDGFEQTDQ QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAILAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLAATAAVE LDGGRAALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LDPKREALRG LDKIIEKPPA
451 GSNTLQAEAL LVQSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNLGY
501 SLLTDSKRLD EGFALLQAY QINPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

	10	20	30	40	50	60
m951.pep	MIMLPNRFKMLTVLTATLIAGQVSAAGGAGDMKQPKVEGKVKFRKQQRYSSEEEIKNERAR					
g951	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKVEGKVKLRKHRRYSSEEEIKNERAR					
	10	20	30	40	50	
	70	80	90	100	110	120
m951.pep	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
	60	70	80	90	100	110
	130	140	150	160	170	180
m951.pep	QAEMIQKWRQIEPIPGKAKRAGWLRNVLRERGNQHLGEEVLAQADEGQNRVFLLL					
g951	QAEMIQKWRQIEPIGKAKRAGWLRNVLRERGNQHLGEEVLAQSDDVQKRRIFLLL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m951.pep	AQAAVQQDGLAQKASKAVRRAALKYEHLPAAVADVFSVQGREKEKAIGALQRLAKLDT					
g951	VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADVFGVQGREKEKAIEALQRLAKLDT					
	180	190	200	210	220	230
	250	260	270	280	290	300
m951.pep	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVWQEMEIMNLVSLRKPDDAYARLNV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m951.pep	LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTEEQRSRAALTAAMMYADRRD					
g951	LLEHNPANLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD					
	300	310	320	330	340	350
	370	380	390	400	410	420
m951.pep	YAKVRQWLKKVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLPEQQGRYFTADNL					
g951	YAKVRQWLKKVSAPEYLFDKGVLA AAAA AVELDGGRAALRQIGRVRKLPEQQGRYFTADNL					
	360	370	380	390	400	410
	430	440	450	460	470	480
m951.pep	SKIQMLALS KL PDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	SKIQMLALS KL PDKREALIGLNNIIAKLSAAGSTEPLAEALAQRSIIYEQFGKRGKMIAD					
	420	430	440	450	460	470
	490	500	510	520	530	540
m951.pep	LERAFRLAPDNAQIMNNLGYSL L TDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	LETALKLTPDNAQIMNNLGYSL L S DSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
	480	490	500	510	520	530
	550	560	570	580	590	600
m951.pep	GDAESALPYLRYSFENDPEPEVA A H LGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	GDAESALPYLRYSFENDPEPEVA A H LGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
	540	550	560	570	580	590
	610					
m951.pep	KRHGIALPQPSRKPRK					
g951	KRYGIALPEPSRKPRKX					
	600	610				

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTTTATCT GTGCTCGCGG CAGCCCTGCT
51  TGC CGG CAG GCGTATGCCG CCGGCGCGGC GGATGCGAAG CCGCCGAAGG
101 AAGTCGGAAG GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAACGAAC GCGCACGGCT TGC GGCAGTG GGCAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCGGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GCGGGAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGGA
451 AATCAGCATC TAGACGGA CTGAGGCTAGG CCGACGAAGG
501 ACAGAACCGG AGGGTGT TTTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCCTTGAGA
601 TATGAACATC TGCCCGAAGC GGC GGTGCC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGACGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAATATC CCGAAATACT CGACGGCTTT TCGAGCAGA CAGACACCCA
801 AAACCTTTCG GCGCTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGAACGC
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CCGCAAACCG
951 AAAAGAAAGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGACGGG GGAACAGCGG GGCAGGGCGG CAATGACGGC GGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
1101 GTCGCGCGCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTCGCGCGG
1151 CTGTCGAGTT GGACGGCGGC AGGGCGGCTT TCGGCGAGAT CCGCAGGGTG
1201 CGGAACTTTC CCGAACAGCA GGGCGGTAT TTTACGGCAG ACAATTTGTC
1251 CAAAATACAG ATGTTGCGCC TGTGAAAGCT GCCCGACAAA CGGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAAC CGCCTGCCGG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAAATGA TTTAGATCT TGAAGGGCGC TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CCTGCTTTCC
1501 GATTCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CCGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCTGTT
1651 GAAAACGACC CCGAGCCCGA AGTTGCCGCC CATTGGGCGC AAGTGTGTTG
1701 GGCATTGGGC GAACGCGATC AGGCGGTGTA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAAACCT CGGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGQ AYAAGAADAK PPKEVGKVFR KQORYSEEEI
51  KNERARLAAY GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDLGLEEV LAQADEGQNR RVFLLLAQAA VQDGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVOGRE KEKAIGALQR LAKLDTEILP PTLMTLRLTA
251 RKYPEILDGF FEQTDTONLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILANRKEG ASVIDGYAEK AYGRGTGEOR GRAAMTAAMI
351 YADRRDYTKV RQWLKKVSAP EYLFDKGVLA AAAVELDGG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLSS
501 DSKRLDEGFA LLQTAYQINP DDTAVNDSIG WAYYLLKGD AE SALPYLRYSF
551 ENDEPEEVAA HLGEVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQSRKPK RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAGQAYAAG--AADAKPPKEVGKVFRKQORYSEEEIKNERAR
          ||| || :|:|:|:|:|:|: ||| | :| | | | | | | | | | | | | | | | |
m951      MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPPKEVGKVFRKQORYSEEEIKNERAR
          10      20      30      40      50      60
a951.pep  LAAGGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
```

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m951      |||||||
          LAAVGERVNIQIFTLGGETALQKQGAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
          70      80      90      100     110     120

a951.pep  120      130      140      150      160      170
          QAEMIYQKWROIPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
m951      |||||||
          QAEMIYQKWROIPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          130      140      150      160      170      180

a951.pep  180      190      200      210      220      230
          AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
m951      |||||||
          AQAAVQQDGLAQKASKAVRRAALKYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          190      200      210      220      230      240

a951.pep  240      250      260      270      280      290
          EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
m951      |||||||
          EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          250      260      270      280      290      300

a951.pep  300      310      320      330      340      350
          LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
m951      |||||||
          LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRSRAALTAAMMYADRRD
          310      320      330      340      350      360

a951.pep  360      370      380      390      400      410
          YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGVRKLEPQQGRYFTADNL
m951      |||||||
          YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGVRKLEPQQGRYFTADNL
          370      380      390      400      410      420

a951.pep  420      430      440      450      460      470
          SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
m951      |||||||
          SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
          430      440      450      460      470      480

a951.pep  480      490      500      510      520      530
          LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
m951      |||||||
          LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
          490      500      510      520      530      540

a951.pep  540      550      560      570      580      590
          GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
m951      |||||||
          GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
          550      560      570      580      590      600

a951.pep  600      610
          KRHGIALPQPSRKPRK
m951      |||||||
          KRHGIALPQPSRKPRK
          610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1      ..TTGTCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTGT
51     TTACGAAAA ATCAAAATTGC AGAGTTGGAA AGCGCGGCGG GATTTCAATA
101    TTGTAAGCA GGATTTGGAT TTTTCCTGCG GGGCGGCTTC GGTGGCGACG
151    CTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTGGA
201    AAAACTGGGT AAGGAACAGA TCGCGCGGTC GTTTGAGGAT ATGCGGCGCA
251    TTATGCCCGA TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301    CAGCTCGCGC AGTTGAAAT CCCCCTCATC GTGTATCTGA AATACGCAA
351    AGACGACCAT TTTTCGGTAT TCGCGGAGT GGATGGCAAT ACGGTTTTCG
401    TTGCCGACCC GTCGCCGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTCG
451    GAGGCTTGGC AAACCCGTGA GGGAAATTG GCAGGCAAAA TTTTGCGCGT
501    CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551    ATCCAAGCGC GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGCGCT

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601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)  
 1 ..LSYRLNAAPM FNDNPVVYVK IKLQSWKARR DFNIVKQDLD FSCGAASVAT  
 51 LLNNFYGQKL TEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE  
 101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL  
 151 EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKRQTE FAVGQVKWWR  
 201 AY\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq  
 1 ATGATGAAGT TCAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT  
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT  
 101 ACGGAAAAAT CAAAGTGCGAG AGTTGGAAAG CGCGGCGGGA TTTCAATATT  
 151 GTAAAGCAGG ATTTGGATT TTTCTGTGG GCGGCTTCGG TGGCGACGCT  
 201 TTGGAACAA TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA  
 251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCAT  
 301 ATGCCTGATT TGGGTTTTGA GGCGAAGGGC TATGCCCTGT CTTTCGAGCA  
 351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG  
 401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT  
 451 GCCGACCCGT CGCTGGGGCA TGTTCGAATG AGCAGGGCGC AGTTTTTGGA  
 501 TGCTTGCAA ACCCGTGAGG GAAATTTGCG AGGTAAGATT TTGGCTGTCA  
 551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC  
 601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC  
 651 AGAGTAA

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep  
 1 MMKFKYVLL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI  
 51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRRI  
 101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDNTVLL  
 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTOH  
 201 PKRQTEFTVG QIRQARAE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

g952.pep	10	20	30	40
	LSYRLNAAPMFNDNPVVYVKIKLQSWKARRDFNIVKQDLDFSCG			
m952	10	20	30	40
	MMKFKYVLLACVVVLSYRLNAAPMFNDNPVVYVKIKVQSWKARRDFNIVKQDLDFSCG			
g952.pep	50	60	70	80
	AASVATLLNNFYGQKL TEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFEQLAQ			
m952	50	60	70	80
	AASVATLLNNFYGQTL TEEVLEKLD KEQMRASFED MRRIMPD LGF EAKGYALSFEQLAQ			
g952.pep	110	120	130	140
	LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPSPGHVSMSRAQFLEAWQTREGNLAGKI			
m952	110	120	130	140
	LKIPVIVYLKVRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFLDAWQTREGNLAGKI			
g952.pep	170	180	190	200
	LAVVPKKA E AISNKLFFTHHPKRQTEFAVGQVKWWRAYX			
m952	170	180	190	200
	LAVIPKKAETISNKLFFTOHPKRQTEFTVGQIRQARAE			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq  
 1 ATGATGAAGT TCAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT

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51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCTCGT TTAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATT CTCCGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTC AATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1 MMKFYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYQTLTEEE VTKKLDKEQM RASFEDMRR
101 MPDLGFCAK YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

	10	20	30	40	50	60
a952.pep	MMKFYVFLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG					
m952	MMKFYVFLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a952.pep	AASVATLLNNFYQTLTEEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ					
m952	AASVATLLNNFYQTLTEEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a952.pep	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFXDAWQTREGNLAGKI					
m952	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFLDAWQTREGNLAGKI					
	130	140	150	160	170	180
	190	200	210	219		
a952.pep	LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAEX					
m952	LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAEX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CCGTCTGACC
151 GGTTCGCTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCGGGA CATCCGCTTC
301 GTTTCACCA AATTCAACTT CAACGGCAAA AACTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAACCT AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```



This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

**g953.pep**  
 1 MKKIIFAALA AAVGTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT  
 51 GSVVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIRF  
 101 VSTKFNENGK KLVSV DGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVCGG  
 151 DFSTTIDRTK WGV DYL V NAG MTKNVRIDIQ IEAAKQ\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

**m953.seq**  
 1 ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC  
 51 CTCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG  
 101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG  
 151 ACCGGTTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT  
 201 CACCATCCCC ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC  
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC  
 301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTCCGTTGA  
 351 CGGCAACCTG ACCATGCACG GCAAACCGC CCCCGTCAA CTCAAAGCCG  
 401 AAAAAATCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC  
 451 GCGCACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT  
 501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG  
 551 CAGCCAAACA ATAA

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

**m953.pep**  
 1 MKKIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL  
 51 TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIR  
 101 FVSTKFNENG KLVSV DGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG  
 151 GDFSTTIDRT KWM DYL V NV GMTKSVRIDI QIEAAKQ\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

**m953/g953** 93.0% identity in 187 aa overlap

	10	20	30	40	50	60
m953.pep	MKKIIFAALAAAAISTASATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
g953	MKKIIFAALAAAAVGTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	
m953.pep	70	80	90	100	110	120
g953	RDGKIDITIPV	ANLQSGSQH	FTDHLKSADI	FDAAQYPDIR	FVSTKFNENG	KKLVSDGNL
	60	70	80	90	100	110
m953.pep	130	140	150	160	170	180
g953	TMHGKTAPVK	LKAEKFNCYQ	SPMEKTEVCG	GDFSTTIDRT	KWGM DYL NV	GMTKSVRIDI
	120	130	140	150	160	170
m953.pep	QIEAAKQX					
g953	QIEAAKQX					

180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

**a953.seq**  
 1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC  
 51 CTCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT  
 101 CTATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG  
 151 ACCGGTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT  
 201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC  
 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC  
 301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTCCGTTGA

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```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GGCGACTTCA GCACCACCAAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYDIR
101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAKEFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

	10	20	30	40	50	60
a953.pep	MKKIIIAALAAAAGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK					
m953	MKKIIFAALAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	60
a953.pep	RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNFNKKLVSVDGNL					
m953	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNFNKKLVSVDGNL					
	70	80	90	100	110	120
a953.pep	RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNFNKKLVSVDGNL					
m953	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNFNKKLVSVDGNL					
	70	80	90	100	110	120
a953.pep	TMHGKTAPVKLKAKEFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
m953	TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	130	140	150	160	170	180
a953.pep	TMHGKTAPVKLKAKEFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
m953	TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	130	140	150	160	170	180
a953.pep	QIEAAKQX					
m953	QIEAAKQX					

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTAACAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAACAGGC TGCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
1  MKKFYFVLLA LGLAACGQEQ SOKADAEQYF FANKYQFADE KOAFYFERAA
51  RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLD KESYQNYRKS MQECKRTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTGT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG GGGGatgaag gcgaacagtc ttgtggtcgg
801 ctatgatgcyg gacggtCtgc CgcaAAaagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaatattatt tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaacc tatcatgcgc aacaaacggt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
1  MFKKFKPVLL SFFALVFAPW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGFLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YNDRPFPSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS VDNKKPKQSV EYYLKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQOTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTGT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACG GTGGATGACG
251 GTCCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CGGGGAAAAA TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATCGG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGCGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCGTGATT TCCTTTGAAC
1051 TTGGAATAAT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
1  MFKKFKPVLL SFFALVFAPW LGTGIAYEIN PRWFLSDTAT EVKPNPNFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGFLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YNDRPFPSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
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251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF  
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN  
 351 LENLEKEVRR YAEAAARRSG GRRDLSH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

g957.pep	10	20	30	40	50	60
m957	10	20	30	40	50	60
g957.pep	70	80	90	100	110	120
m957	70	80	90	100	110	120
g957.pep	130	140	150	160	170	180
m957	130	140	150	160	170	180
g957.pep	190	200	210	220	230	240
m957	190	200	210	220	230	240
g957.pep	250	260	270	280	290	300
m957	250	260	270	280	290	300
g957.pep	310	320	330			
m957	310	320	330	340	350	360
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATCAAACC	GGTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAACTT
151	GCCCCCTGT	TCCGAAATGC	CGACAGGCGG	GTTGTATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TGCCCAGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCCAGGTA	TATTGGCGGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAACAGT	CTTGTGTCG	GCTATGATGC
801	GACCGGCTG	CCGAGAAAG	TCTATTGGAG	TTTCGACAA	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

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951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTTCGGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1 MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL POKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50
m957	10	20	30	40	50
a957.pep	60	70	80	90	100
m957	60	70	80	90	100
a957.pep	120	130	140	150	160
m957	120	130	140	150	160
a957.pep	180	190	200	210	220
m957	180	190	200	210	220
a957.pep	240	250	260	270	280
m957	240	250	260	270	280
a957.pep	300	310	320	330	340
m957	300	310	320	330	340
a957.pep	360	370			
m957	360	370			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1 TTGGCTCGTT TATTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51 TTTCGGCAGC CATTGCGCCG CCGATACCGT TGCGGCGGAA GAGGCGGACG

```

```

101 GGCCTGTGCG AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAAGCT
151 TCCGATTGTA CCCTCGGTTT GACCTGCCTG TTTTGAGTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCAGAG CCGCCGTCCA AGGACGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGGGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTCCGC CTCCAACAGG ACGGTACGCT GATTGCGGGC
451 GAAACCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACGT
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCTAATC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCTTCG
701 TGTTCCGCGG CGTTCCTCTT TTCTATACGC CTGCGCGGA CTTCCTCGTT
751 GACGGCAACC GCAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCGGTTTC
801 GGACGGCGTT TCCCTTTCCG TCCCTATTA TTCAACCTT GCCCCAACT
851 TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGACAAAT TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCAG GCGGCGGGGA GGCAGCCTGA ATGCCGCGCT TTCGTTTCAG
1201 AAATACCAGA CGCTGGCAA CCAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCGCT TCAGCCACGA CGGCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTAGCAA
1401 CAGCTGGGGC TACGTCCGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGCGG AAAGCATCCC GCAGCGTCGG GCGCGTTTTG
1501 CCGGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAAC
1601 ATATTCCTGC CAAATCTCAA AACGACCTGC CCAATTTCTA TTCGTGCGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCA ACAGCCTTTC CACCGCCGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTAG
1801 AAATCTTATT TCAAGGATGA TCGGTTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTCGCCTCC GCGGCGATAG
1901 CGGGCGGTTT CACCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCCG CCCCAGGAAA
2001 AGTGTGGAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTGCTCC GCTACAATA
2151 CCGGTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG GTTACGCCCA ACGTACGTT
2251 ACCGCGGAAA ACACCTACAA AAACGCCGTC TTTTTCCTAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCGCG AGGACGGATG GATGTCGCGC
2351 TTCCCGGCTA CATCCCGGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

g958.pep

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1 LARLFSLKPL VIALGFCEFGT HCAADTVAAE EADGRVAEGG AQAASESAQA
51 SDLTGLSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQQDGLIRG
151 ETLTYNLDQQ TGEAHNVRME TEQGGRLQS VSRTEMLGE GRYKLTETQF
201 NTCASGDAGW YVKAASVEAD RKGIGVAKH AAFVFGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRPD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFNSWVG YVRPKLGLHA TYSLDSFGG KASRSVGRVL
501 PVVNIIDGGTT FERNTRLFGG GVVQTIEPRL FYNYIPAKSQ NDLPNFDSSSE
551 SSFGYQGLFR ENLYYGNDRI NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSVGKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLQADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLQLKDLS SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

m958.seq

```

1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTCTGT
51 CTTGCGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGCCGA ACCCATACAG

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1371

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
351 GACGACCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACGTAC GGAACCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTCAAGGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCG
701 TCGTGTTCGG CGGCGTTCCC ATTTCTACA CCCCTTGGGC GGAATTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTGCGAGCGG GTTTCCTTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CTTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC ACAAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGCGGGCG GCGGGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CCGTCGAGTG GCGTAAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCGCA CAATTTACCC GATTACGCCA CGACAGCCGC
1351 CAAGACGGCA GCGCCCTGGT CGTCTATCCC GACATCAAAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATTT TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTTCGG GGAGAAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTTCGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCGCGCCGC GTGCAAAGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGT
1801 CAGAAATCTT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCC CGCAACCGTT CCGACTGGGT GGCATTGGCC TCCGGCAGCA
1901 TCGGCGAGCC CTTTCATCCT GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAAGTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTT AACGCCCCGT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAGG TTGCGGCTGC TGGGCGCGG GCGTGTACGC CCAAGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GAGAAACCC CGCAGACAGG ATGGATGTG
2351 CCGTTCGCCG CTATATCACC GCCCACCTC TTTCCGCCG ACGCAACAAA
2401 CGACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1  LARLFLSKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51  PLSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMGQ
101 SQVQVRAEGN VVVERNRTL NTDWADYDQS GDTVTAGDRF ALQQDGLTLR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLO SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVFGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VLSVPPYFN LAPNLDAFPA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIIDSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGVSQKKP RNRSDWVAFS SGISGRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVKLV NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLA GAEYKSSCGC WGAGVYAORY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRKN
801  RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

[illegible]



1373

	730	740	750	760	770	780
m958.pep	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	:     :     :     :     :     :					
g958	EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR					
	720	730	740	750	760	770

  

	790	800
m958.pep	MDVAVPGYITAHSLSAGRNRKP	
	:     :     :	
g958	MDVAVPGYIPAHSLSAGRNRKP	
	780	790

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

a958.seq

1	TTGGCTCGTT	TATTTTCACT	CAAACCACTG	GTGCTGGCAT	TGGGCTTCTG
51	TTTTCGGCAGC	CATTGCGCCG	CCGCCGATGC	CGTTGCGGCG	GAGGAAACGG
101	ACAATCCGAC	CGCCGGAGGA	AGCGTTCGGA	GCGTGTCGGA	ACCCATACAG
151	CCTACCCAGCC	TGAGCCTCGG	TTCGACCTGC	CTGTTTGTGA	GTAACGAAAG
201	CGGCAGCCCC	GAGAGAACCG	AAGCCGCCGT	CCAAGGCAGC	GGCGAAGCAT
251	CCATCCCCGA	AGACTATACG	CGCATTGTGT	CCGACAGGAT	GGAAGGACAG
301	TCGCAGGTGC	AGGTGCGTGC	CGAAGGCAAC	GTCGTCGTCG	AACGCAATCG
351	GACGACCCTC	AATGCCGATT	GGGCGGATTA	CGACCAGTCG	GGCGACACCG
401	TTACCGCAGG	CGACCGGTTC	GCCCTCCAAC	AGGACGGTAC	GCTGATTCGG
451	GGCGAAACCC	TGACCTACAA	TCTCGAGCAG	CAGACCGGGG	AAGCGCACAA
501	CGTCCGTATG	GAAACCGAAC	ACGGCGGACG	GCGGCTGCAA	AGCGTCAGCC
551	GCACCGCCGA	AATGTTGGGC	GAAGGGCATT	ACAAACTGAC	GGAAACCCAA
601	TTCAACACCT	GTTCCGCCGG	CGATGCCGGC	TGGTATGTCA	AGGCCGCTTC
651	CGTCGAAGCC	GATCGGGAAA	AAGGCATAGG	CGTTGCCAAA	CACGCCGCCT
701	TCGTGTTCCG	CGGCGTTCCC	ATTTTCTACA	CCCCTTGGGC	GGACTTCCCG
751	CTTGACGGGA	ACCGCAAAAG	CGGCCTGCTC	GTTCCCTCAC	TGTCCGCCGG
801	TTCGGACGGC	GTTTCCCTTT	CCGTTCCTTA	TTATTTCAC	CTTGCCCCCA
851	ATCTCGATGC	CACGTTTCGG	CCCGGCGTGA	TCGGCGAAGC	CGGCGCGGTC
901	TTTGACGGGC	AGGTACGCTA	CCTGCGGCCG	GATTATGCCG	GCCAGTCCGA
951	CCTGACCTGG	CTGCCGCACG	ACAAGAAAAG	CGGCAGGAAT	AACCGCTATC
1001	AGGCGAAATG	CGAGCACCGG	CACGACATTT	CCGACACGCT	TCAGGCGGGT
1051	GTCGATTTC	ACCAAGTCTC	CGACAGCGGC	TACTACCGCG	ACTTTTACGG
1101	CAACAAAGAA	ATCGCCGGCA	ACGTCAACCT	CAACCGCCGT	GTATGGCTGG
1151	ATTATGGCGG	CAGGGCGGCG	GGCGGCAGCC	TGAATGCCCG	CCTTTCGGTT
1201	CTGAAATACC	AGACGCTGGC	AAACCAAAGC	GGCTACAAAG	ACAAACCGTA
1251	TGCCCTGATG	CCGCGCCTTT	CCGCCGATTG	GCGCAAAAAC	ACCGGCAGGG
1301	CGCAAAATCG	CGTGTCGCC	CAATTTACCC	GCTTCAGCCA	CGACAGCCGC
1351	CAAGACGGCA	GCCGCCTCGT	CGTCTATCCC	GACATCAAA	GGGATTTTCAG
1401	CAACAGCTGG	GGTACGTCC	GTCCCAAACT	CGGACTGCAC	GCCACCTATT
1451	ACAGCCTCAA	CCGCTTCGGC	AGCCAAGAAG	CCCGACGCGT	CAGCCGCACT
1501	CTGCCCATCG	TCAACATCGA	CAGCGGCATG	ACCTTCGAAC	GCAATACGCG
1551	GATGTTCCGG	GGCGGAGTCC	TGCAAAACCT	CGAGCCGCGC	CTGTTCTACA
1601	ACTATATTCC	TGCCAAATCC	CAAAACGACC	TGCCCAATTT	CGATTTCGTCG
1651	GAAAGCAGTG	TCGGCTACGG	GCAGCTTTT	CGTGAAGAAC	TCTATTACGG
1701	CAACGACAGG	ATTAACACCG	CAAACAGCCT	TTCGCGCCGC	GTGCAAGAGC
1751	GTATTTTGGA	CGGCGCGACG	GGGGAAGAGC	GTTTCGCGCG	CGGCATCGGG
1801	CAGAAATTCT	ACTTCAAAA	CGACGCAGTC	ATGCTTGACG	GCAGTGTCGG
1851	CAAAAACCGC	CGCAGCCGTT	CCGACTGGGT	GGCATTTCGCC	TCCAGCGGCA
1901	TCGGCAGCCG	CTTCATCCTC	GACAGCAGCA	TCCACTACAA	CCAAAACGAC
1951	AAACGCGCCG	AGAACTACGC	CGTCGGTGCA	AGCTACCGTC	CCGCACAGGG
2001	CAAAGTGCTG	AACGCCCGCT	ACAAATACGG	GCGCAACGAA	AAAATCTACC
2051	TGAAGTCCGA	CGGTTCCCTAT	TTTACGACA	AACTCAGCCA	GCTCGACCTG
2101	TCCGCACAAT	GGCCGCTGAC	GCGCAACCTG	TCGGCCGTCG	TCCGTTACAA
2151	CTACGGTTTT	GAAGCCAAA	AACCGATAGA	GGTGCTGGCG	GGTGCGGAAT
2201	ACAAAAGCAG	TTGCGGCTGC	TGGGGCGCGG	GCGGTGTACG	CCAACGCTAC
2251	GTTACCGGCG	AAAACACCTA	CAAAAACGCT	GTCTTTTCT	CACTTCAGTT
2301	GAAAGACCTC	AGCAGTGTCG	GCAGAAACCC	CGCAGACAGG	ATGGATGTCG
2351	CCGTTCCCGG	CTATATCCCC	GCCCACTCTC	TTTCCGCCGG	ACGCAACAAA
2401	CGGCCCTGA				

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

a958.pep

1	LARLFSKLP	VLALGFCFGT	HCAAADAVAA	EETDNPTAGG	SVRSVSEPIQ
51	PTSLSLGSTC	LFCSNESGSP	ERTEAAVQGS	GEASIPEDYT	RIVADRMGGQ
101	SQVQVRAEGN	VVVERNRTTL	NADWADYDQS	GDTVTAGDRF	ALQDGTLLR
151	GETLTYNLEQ	QTGEAHNVRM	ETEHGGRRLQ	SVSRTAEMLG	EGHYKLTETQ
201	FNTCSAGDAG	WYVKAASVEA	DREKGIGVAK	HAAFVFGGVP	IFYTPWADFP

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251 LDGNRKSGLL VPSLSAGSDG VSLSVPPYYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSGVKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GA EYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRKN
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

	10	20	30	40	50	60
a958.pep	LARLFS	LKPLVL	ALGFCF	GTHCAA	ADAVAA	EETDNPTAGGSVRSVSEPIQPTSLSLGSTC
m958	LARLFS	LKPLVL	ALGFCF	GTHCAA	ADAVAA	EETDNPTAGESVRSVSEPIQPTSLSLGSTC
	10	20	30	40	50	60
a958.pep	LFCSNE	SGSPER	TEAAVQ	GSGEAS	IPEDYTR	IVADRM
m958	LFCSNE	SGSPER	TEAAVQ	GSGEAS	IPEDYTR	IVADRM
	70	80	90	100	110	120
a958.pep	EGSQVQ	VRAEGN	VVVERN	RTTL		
m958	EGSQVQ	VRAEGN	VVVERN	RTTL		
	70	80	90	100	110	120
a958.pep	NADWAD	YDQSGD	TVTAGD	RFALQD	GTGTLR	GETLTYN
m958	NTDWAD	YDQSGD	TVTAGD	RFALQD	GTGTLR	GETLTYN
	130	140	150	160	170	180
a958.pep	LEQQTGE	AHNVRM	ETEHGG	RRLQ		
m958	LEQQTGE	AHNVRM	ETEHGG	RRLQ		
	130	140	150	160	170	180
a958.pep	SVSR	TAEM	LGEGHY	KL	TETQ	FNTCSA
m958	SVSR	TAEM	LGEGHY	KL	TETQ	FNTCSA
	190	200	210	220	230	240
a958.pep	GAGWYV	KAASVE	ADREK	GIGV	AKHAA	FVFGGVP
m958	GAGWYV	KAASVE	ADREK	GIGV	AKHAA	FVFGGVP
	190	200	210	220	230	240
a958.pep	IFYTPW	ADFP	LDGNRK	SGLLV	VPSLSA	GDGVSL
m958	IFYTPW	ADFP	LDGNRK	SGLLV	VPSLSA	GDGVSL
	250	260	270	280	290	300
a958.pep	SVPPYY	FN	LAPN	LDAT	FAPG	VIGERGAV
m958	SVPPYY	FN	LAPN	LDAT	FAPG	VIGERGAV
	250	260	270	280	290	300
a958.pep	FDGQV	RYLRP	DYAGQ	SDLTW	LPHDKK	SGRNNR
m958	FDGQV	RYLRP	DYAGQ	SDLTW	LPHDKK	SGRNNR
	310	320	330	340	350	360
a958.pep	YQAKWQ	HRHDIS	DTLQAG	VDFN	QVSDSG	
m958	YQAKWQ	HRHDIS	DTLQAG	VDFN	QVSDSG	
	310	320	330	340	350	360
a958.pep	YYRDF	YGNKEI	IAGNVN	LNRRV	WLDYGG	RAAGGS
m958	YYRDF	YGNKEI	IAGNVN	LNRRV	WLDYGG	RAAGGS
	370	380	390	400	410	420
a958.pep	SLNAGL	SVLKYQ	TLANQS	GYKDK	KPYALM	
m958	SLNAGL	SVLKYQ	TLANQS	GYKDK	KPYALM	
	370	380	390	400	410	420
a958.pep	PRLSAD	WRKNTG	RAQIGV	SAQFTR	FSHDSR	QDGSRL
m958	PRLSAD	WRKNTG	RAQIGV	SAQFTR	FSHDSR	QDGSRL
	430	440	450	460	470	480
a958.pep	VVYPDI	KWDFS	NSWGY	VRPKL	GLH	
m958	VVYPDI	KWDFS	NSWGY	VRPKL	GLH	
	430	440	450	460	470	480
a958.pep	ATYYSL	NRFSGE	ARRVSRT	LPIVN	IDSGMT	FERNTR
m958	ATYYSL	NRFSGE	ARRVSRT	LPIVN	IDSGMT	FERNTR
	490	500	510	520	530	540
a958.pep	MFGGGV	LQTLEP	RFLFY	NIYIPAKS		
m958	MFGGGV	LQTLEP	RFLFY	NIYIPAKS		

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	490	500	510	520	530	540
	550	560	570	580	590	600
a958.pep	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a958.pep	QKFYFKDDAVMLDGSVGKKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKDDAVMLDGSVGKKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
	670	680	690	700	710	720
a958.pep	SYRPAQGVNLNARYKYGRNEKIYKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRNYGFG					
m958	SYRPAQGVNLNARYKYGRNEKIYKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRNYGFG					
	670	680	690	700	710	720
	730	740	750	760	770	780
a958.pep	EAKKPFEVLGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
m958	EAKKPFEVLGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
	790	800				
a958.pep	MDVAVPGYIPAHSLSAGRNRKRPX					
m958	MDVAVPGYITAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDHGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAARAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDHGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

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m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MNIKHL	LLTSAAT	LLSISAP	ALAHHD	GHGDD	DHGHAAHQHNKQDKIISRAQAEKAALAR
g959	MNIKHL	LLTAAAT	LLGISAP	ALAHHD	GHGDD	DHGHAAHQHGKQDKIISRAQAEKAAR
	10	20	30	40	50	60
	70	80	90	100	109	
m959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEY	KVVVDARTGRVISSRRDDX
g959	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEY	KVVVDARTGRVISSRRDDX
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

1	ATGA	ACTTCA	AACGC	CTTCT	CTTGAC	CGCC	GCCGCA	ACCG	CACTG	ATGGG
51	CATT	TCCGCC	CCCGC	ACTCG	CCCACC	CACGA	CGGAC	ACGGC	GATGAC	GACC
101	ACGG	ACACGC	CGCAC	ACCAA	CACAG	CAAA	AAGACA	AAAT	CATCAG	CCGC
151	GCCCA	AGCCG	AAAA	AGCAG	GTTGG	CGCGT	GTCGG	CGGCA	AAATC	ACCGA
201	CATCG	ATCTC	GAAC	CACACA	ACGGC	CGTCC	GCACT	ATGAT	GTCGAA	ATCG
251	TCAAA	AACGG	ACAGG	AATAC	AAAGT	CGTTG	TCGAT	GCCCC	TACCG	CGCCG
301	GTGAT	TTCT	CCGCC	CGCA	CGACT	GA				

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

1	MNFK	RLLLTA	AATAL	MGISA	PALAH	HDGHG	DDDHG	HAAHQ	HSKQD	KIISR
51	AQAE	KAALAR	VGGKI	TIDL	EHNGR	PHYD	VEIVK	NGQEY	KVVVD	ARTGR
101	VISS	RRDD*								

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MNFKRL	LLTAAAT	ALMGISA	PALAHHD	GHGDD	DHGHAAHQHSKQDKIISRAQAEKAALAR
m959	MNIKHL	LLTSAAT	LLSISAP	ALAHHD	GHGDD	DHGHAAHQHNKQDKIISRAQAEKAALAR
	10	20	30	40	50	60
	70	80	90	100	109	
a959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEY	KVVVDARTGRVISSRRDDX
m959	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEY	KVVVDARTGRVISSRRDDX
	70	80	90	100		

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

1	ATGC	AAGTAA	ATATT	CAGAT	TCCCT	GTATG	CTGTAC	AGAC	GCGGG	AGTGT
51	TAAG	CCCCC	TTGTT	TGAAG	CTCCG	CGGCT	CCTGCC	GAGC	TTCACC	GACC
101	CCGT	TGTGCC	CAAGC	TCTCT	GCTCC	CGGCG	GCTAC	ATTGT	CGACAT	CCCC
151	AAAG	CAATC	TGAAA	ACCGA	AATCG	AAAAG	CTGGC	CAAA	AGCCCC	GAGTA
201	TGCC	TATCTG	AAAC	AGCTCC	AAGTA	AGCGAA	AAAC	GTCAAC	TGGAAC	CAGG
251	TGCA	ACTGGC	TTAC	GATAAA	TGGGA	CTATA	AGCAG	GGAAG	CTTAAC	CAGA
301	GCCG	TGCAG	CGATT	ATCGC	GCTGG	CTGTT	ACCGT	TGGTTA	CTGCG	GGGCG
351	GGGAG	TCGGA	GCCGC	ACTAG	GCTTA	ACGG	CGCAG	CCGCA	GCAGC	GGCCG
401	ATGC	CGCCT	TGCT	CACTC	GCTTC	TCAGG	CTTCC	GTATC	GCTCAT	CAAC
451	AATA	AAGCG	ATGTC	GGCAA	AACCC	TGAAG	GAAC	TGGCA	GAAGC	CGCAC
501	GGTA	AAAAAT	CTGGT	TGTAG	CGCGG	CAAC	GCCAG	GCGTA	TCCAAC	AAAC

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551 TCGGTGCTCT TCCCTTGCC ACTTGAGCG AAACCCCTTG GTTAAACAAC
601 CTCAACGTTA ACCTGGCCAA TCGGGGCGAGT GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCC CAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTCGGG GAGGCTTTGG TTAAAAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAACGCGG TAGAAAATAA TGCGGTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCTG CGAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTAG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGAAAAA CAGCTGGCTC AATTTTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGCTCTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATT AGATGGCCAA
1501 CATAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTTCG TTAACCAAA GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLPS FTDPVVPKLS APGGYIVDIP
51 KGNLKEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDKQEGLTR
101 AGAAIIALAV TVVTTAGAGVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKN LVVAAATAGV SNKLGLASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEAAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLFDETL
401 LDWDAKVID IVVGTGLNRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPEFG QLAQISEKTT LPTQQGSQVF LVKRNQGLLK TGDRFYLDGQ
501 HKNHLEVFDK NGNFKFVLNM DGSLNQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAAAAACA AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGTA AGAGACTAAG ACAATATATG TAAAAATTGA
501 TGA AAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGCCGGAAG AAACCAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGCCG
701 AAGCTGCCGC TGGCAGAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCCG TTCAATGTAA CGGCTGCAGT
951 CGGCGGCTAC AAATCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTGCGGCTC AATTACGAGT GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPKLV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

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1378

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKVKA AETA A GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTA AVGGY KSESAVAIGT GFRETENFAA KAGVA VGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet

a961.pep not found yet

g972.seq not found yet

g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

m972.seq

```

1  TTGACTAACA GGGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTAC ATCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GATGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAAAT CTCGTTTTGT TCGTGTTTAT GAGAAAAGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTTCG GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAG AAAATTAAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCCGGGAT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

m972.pep

```

1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGKLEIP QRRGKQDGVF
51  VDWSIFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLVNFMIE M GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

a972.seq

```

1  TTGACTAACA GGGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTAC ATCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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1379

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTTCAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTG GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCGAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATTT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATCTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
  1 LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKKGKLEIP QRRGKQDGVF
  51 VDWISFTFHE DTLKLVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
 101 GNKFYESMYR LGSDDVDYGE VHFQGGQRNTV LVELKGTGCS VASPGWELRL
 151 KQFLDDSIPT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
 201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
 251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTNLNLTFE
 301 HKLHYAKNAV GKLVNFMIEI GFDNSEIVES LKADSGFPKG LEPEKYALEM
 351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPTYDVE
 401 KERKQYEYLS KVIHQNVVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLK	TXSKSSERMS	EVEYFSHFIS	DGKKGKLEIP	QRRGKQDGVF	VDWISFTFHE
a972	LTNRGGAKLK	TNSKSSERMS	EVEYFSHFIS	DGKKGKLEIP	QRRGKQDGVF	VDWISFTFHE
	70	80	90	100	110	120
m972.pep	DTLLKVS	GCP	LFSDAEYMYV	LSRKLEEILG	FGITRKCKSR	GNKFYESMYR
a972	DTLLKVS	GCP	LFSDAEYMYV	LSRKLEEILG	FGITRKCKSR	GNKFYESMYR
	130	140	150	160	170	180
m972.pep	VHFGXQRNTV	LVELKGTGCS	VASPGWELRL	KQFLDDSIPT	RITRIDLALD	FFDGEYTPDQ
a972	VHFGGQRNTV	LVELKGTGCS	VASPGWELRL	KQFLDDSIPT	RITRIDLALD	FFDGEYTPDQ
	190	200	210	220	230	240
m972.pep	ALLDHDNGFF	DNSNQRPKSE	TIGTAWRNED	GSGKTFYVGR	KKNSRFVRVY	EKGRQLGDKE
a972	ALLDHDNGFF	DNSNQRPKSE	TIGTAWRNED	GSGKTFYVGR	KKNSRFVRVY	EKGRQLGDKE
	250	260	270	280	290	300
m972.pep	SKWVRFEIQF	NYGDIEIPLD	ILINQGSYFC	GAFFPICRKF	NMPVPERFDQ	RKKTNLNLTFE
a972	SKWVRFEIQF	NYGDIEIPLD	ILINQGSYFC	GAFFPICRKF	NMPVPERFDQ	RKKTNLNLTFE

1380

	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDRKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDRKRLFSPDYDVEKERKYQEYLSKVYHQNVDDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCC
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCGGTACG GAatacggca gcgaagaagc cgacaccatc ggcggtTGG
701 TCATTACAGG ATTGGGACAC CTGCCCCTGC GCGGCGAAAA AGTCCTTAtc
751 ggcgGTTTGC agttcacgct CGCCCCGCGC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFPGT EYGSEADTI GGLVIQELGH LPVRGEKVLI
251 GGLQFTVARA DNRRLLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCC
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTTA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCGCCGTCT
401 TCGTCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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1381

651 CTTCGGCACG GAATACAGCA kCGAAGAAGC CGACACCATT GGCGGCCTGG  
 701 TCATTCAAGA GTTGGGACAT CTGCCCCTGC GCGGCGAAAA AGTCCTTATC  
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC  
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973 .pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE  
 51 KVLDFSLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED  
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE  
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS  
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL  
 251 GGLQFTVARA DNRRLHTLMA TRVK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

	10	20	30	40	50	60
m973 .pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSLEV					
	:					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFAELEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973 .pep	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	:					
g973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973 .pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	:					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973 .pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGT EYSXEEADTI GGLVIQELGH					
	:     :     :     :     :					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFGT EYGSEEADTI GGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973 .pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	:					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973 .seq

1 ATGGACGGCG CACAACCGAA AACAAATTT TTTGAACGCC TGATTGCCCG  
 51 ACTCGCCCGC GAACCGGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC  
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA  
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG  
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG  
 251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCGTCAT CGGTGAAGAC  
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT  
 351 GTTCAACCCC GAGCAGTTC ACCTCAAATC GATATTGCGC CCTGCCGTCT  
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA  
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG  
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG  
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

1382

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GCGCGCCTGG
701 TCATTTCAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GCGGTTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLE
  51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLV FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
 201 ERWRIHAATE IEDINAFFGT EYSSEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSDLEV					
	:					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
	:     :     :     :					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFFGTEYSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCAC TCGCGCTGTC
  51 TGCCTGCGGC GGTCAAGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
 101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
 151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
 201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
 251 ACAGCCTTTT CCCCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
 301 GCGGTAAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
 351 GTATTTTGAA ATCACCACAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
 401 CTTCCTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
 451 CACACGGGCG ATTTCTCCGT TTCCAACTC TTGGGCAACG ACAATCCGAA
 501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAGAA CTGGAAAACG
 551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
 601 AAAAACAACC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
 651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
 701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
 751 AAGATCTACG CCAAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

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1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```
g981.pep
1   MKKWIAAALA CSALALSACG GQGKDAAPA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK MNKVGVTG
151 HTGDFSUSKL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPAKGMDV VTLPDFTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```
m981.seq
1   ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAGGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTA AACACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACCGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAACGAC
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAACAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```
m981.pep
1   MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK MNKVGVTG
151 YTGDFSUSKL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPAKGMDV VTLPDFTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/g981 98.1% identity in 266 aa overlap

```

      10      20      30      40      50      60
981.pep  MKKWIAAALAC SALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
          |||
g981     MKKWIAAALAC SALALSACGGQGKDAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF
          |||

      10      20      30      40      50      60
981.pep  DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE
          |||
g981     DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE
          |||

      130     140     150     160     170     180
981.pep  ITQVVLVPKGKKVSSSEDLKMNKVGVTGYTGDFSUSKLLGNDNPKIARFENVPLIIE
          |||
g981     ITQVVLVPKGKKVSSSEDLKMNKVGVTGHTGDFSUSKLLGNDNPKIARFENVPLIIE
          |||

      190     200     210     220     230     240
981.pep  LENGGLDSVVS DSAVIANVVKNNPAKGMDVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
          |||
g981     LENGGLDSVVS DSAVIANVVKNNPAKGMDVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
          |||

      250     260
981.pep  EKVRESGEYDKIYAKYFAKEDGQAAKX
          |||
g981     EKVRESGEYDKIYAKYFAKEGGQAAKX
          |||
```

1384

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGT CAGGGTA AAGATGCCGC CGCGCCCGC GCAAATCCCC
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCC GCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACC AAG TCGTCCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGG TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQGKDAAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKGVVVTG
151 YTGDFS VSKL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIAN YV
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALAC SALALSACG GQGKDAAAPAANPDKVYRVASNAEFAPFES LDSKGNVEGF					
a981	MKKWIAAALAC SALALSACG GQGKDAAAPAANPDKVYRVASNAEFAPFES LDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	ITQVVLVPKGK KKVSSSEDLK NMNKGVVVTGYTGDFS VSKLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPKGK KKISSSEDLK NMNKGVVVTGYTGDFS VSKLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	ITQVVLVPKGK KKVSSSEDLK NMNKGVVVTGYTGDFS VSKLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPKGK KKISSSEDLK NMNKGVVVTGYTGDFS VSKLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	LENGGLDSVVSDSAVIAN YVKNPKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVSDSAVIAN YVKNPKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	LENGGLDSVVSDSAVIAN YVKNPKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVSDSAVIAN YVKNPKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	EKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				
m981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	EKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1  atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgcCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCC CCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAGT CGCGTCCAAA ACCAAcgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAAGgca TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTT TTGCTGTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGCGC ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTtccGAAG Aagtcggcct GTCTTTGGAA AAAGcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaacact ACCGTCATcg
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAACCTGGCAG GAGGCGTGGC AGTGATCAAA GTCGGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TCGCGCGCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTAtc GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGGAAT GGGCGGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1  IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAKPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV L LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI L KTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENLH TGNADQDAGV QIVLRAVES P
451 LRQIVANAGG EPSVVVNKVL EGKNGYGYNA GSGEYGMIG MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGGM GMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1  ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCC CCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAGT TCGGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGGAAGAAA CAAATCGCTG CTTTGACAA

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1386

```

651 TCCGTTTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCTGGC TTCGGCGACC
851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCGCCG TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA GTGAA

```

This corresponds to the amino acid sequence <SEQ ID 2964; ORF 982>:

```

m982.seq
  1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
  51 AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TGGGGCCCCA
 101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
 151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
 201 AAATATGGGC GCGCAAATGG TGAAGAAGT TCGCTCCAAA ACCAACGACG
 251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
 301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
 351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
 401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
 451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
 501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
 551 AAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
 601 TCTCCTTACT TCATCAACGA TCGGAAAAAA CAAATCGCTG CTTTGGACAA
 651 TCCGTTTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
 701 TGCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
 751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
 801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCTGGC TTCGGCGACC
 851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
 901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
 951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCGCCG TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA GTGAA

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m982/g982    95.8% identity in 544 aa overlap

              10      20      30      40      50      60
m982.pep    MAAKDVQFGNEVRQKMNVGNNILANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI
              :|:::|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

1387

g982	IASQNLRFDNRFLQKMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVEVASKTNDVAGDGTATTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVEVASKTNDVAGDGTATTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVAVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVAVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq	1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAAATGGT
	51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
	101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCC	GCACATCACC
	151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAAGTCAAAG	ACAAGTTTGA
	201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	GCGGTCCAAA	ACCAACGACG
	251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
	301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCGA	CCGACCTGAA
	351	ACGCGGTATC	GACAAAGCCG	TCGCGGCTTT	GGTTGAAGAG	CTGAAAAACA

1388

```

401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTG TTGCTGTTTC ACAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTGC CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGCGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGCCG
1151 CGACCGAAGT GGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGTTGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGCGGCAT GGGTGGTATG GGCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

a982.pep

```

1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFLDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGTV
301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVNVKVL EGKGNYGYN A GSGEYDMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GMM*

```

m982/a982 99.3% identity in 544 aa overlap

```

          10      20      30      40      50      60
m982.pep  MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          |||
a982      MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          10      20      30      40      50      60

          70      80      90      100     110     120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          |||
a982      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          70      80      90      100     110     120

          130     140     150     160     170     180
m982.pep  DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          |||
a982      DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m982.pep  KLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
          |||
a982      KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
          190     200     210     220     230     240

```



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	250	260	270	280	290	300
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNKVLEGGKNGYGYNA					
a982	RARAALLENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNKVLEGGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAAGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTTC	AACGCCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTT
501	GGATGTCCAA	TCCGATGTGC	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTGCGTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTGCGC	ATCAATCCGG	GCAATTCGGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTCAAGG	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGGCGCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

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1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep

```

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSNAETDS DPLADSDPFY
101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGMCSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq

```

1 GTGTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
51 GCTGGCAGGC TGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
301 GAATTTTTCA AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GGCGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGTACAT CCTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGCGCGGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CATCGTGTCG GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC GCACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGCGGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGCGGCGG CACTGATTGC CAAAATCCTG CCGGCGAGCC
1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCAATCC GCAGGCATTA CCCTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep..

```

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSNAENDS DPIADNDPFY
101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGMCSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**m986/g986** 97.0% identity in 499 aa overlap

m986.pep	10	20	30	40	50	60
	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
m986.pep	70	80	90	100	110	120
	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
m986.pep	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMSGIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMSGIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
m986.pep	250	260	270	280	290	300
	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVI IQEVS YGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVI IQEVS YGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHTDSSGKHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCCTC
51  GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACTG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAAGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCCG
951 TTTGGACAAA GCCGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPNM PEIPEEADD GGLNFGSGFI ISKDG YILTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ

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1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD  
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS  
 401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGHLVVVR VSDAERAGL  
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ\*

m986/a986 98.2% identity in 499 aa overlap

m986.pep	10	20	30	40	50	60
a986	10	20	30	40	50	60
m986.pep	70	80	90	100	110	120
a986	70	80	90	100	110	120
m986.pep	130	140	150	160	170	180
a986	130	140	150	160	170	180
m986.pep	190	200	210	220	230	240
a986	190	200	210	220	230	240
m986.pep	250	260	270	280	290	300
a986	250	260	270	280	290	300
m986.pep	310	320	330	340	350	360
a986	310	320	330	340	350	360
m986.pep	370	380	390	400	410	420
a986	370	380	390	400	410	420
m986.pep	430	440	450	460	470	480
a986	430	440	450	460	470	480
m986.pep	490	500				
a986	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq  
 1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG

1394

```

51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTT
351 ggacgacaAC AACAcgcgcg gcttgagca tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtctg CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTTCGACCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAAGGACG GCATAGACGT TACCGTCTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACCT TACGAGCTGC
1151 AACCACAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAACGCA TCGCCGAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLLCSCSSW LPPLERTES RHFNTSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERG VRVRLLEDN NTRGLDLLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 TSVSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

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m987.seq
1  ATGAAACAC GCAGCCTAAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTTCGACCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCCA
951 AAAAAGCGTC TATCTGGTTT CACCTATTT CGTTCCACACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCACAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGGT TCGTTCAACC TCGACCCCCG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1 MKTRSLISLL CLLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAAERG VVRVRLDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m987/g987 97.8% identity in 508 aa overlap

          10      20      30      40      50      60
m987.pep  MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY
          |||
g987       MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDNLQIRHTPHNNGLSDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m987.pep  LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLDDN
          |||
g987       LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLDDN
          70      80      90      100     110     120

          130     140     150     160     170     180
m987.pep  NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
          |||
g987       NTRGLDDLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
          130     140     150     160     170     180

          190     200     210     220     230     240
m987.pep  LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHSAHNATRIIRSGDIG
          |||
g987       LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHSAHNATRIIRSGNIG
          190     200     210     220     230     240

          250     260     270     280     290     300
m987.pep  KGLQALGYNDETSRHALLRYRETVEQSPYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR
          |||
g987       KGLQALGYNDETSRHALLRYRETVEQSPYQKIQTGRIDWQSVQTRLISDPAKGLDRDR
          250     260     270     280     290     300

          310     320     330     340     350     360
m987.pep  RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL TNSLQATDVA

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1396

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|||||
g987      RKPP|IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDIVTVLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNLQWHPATRK
          |||||
g987      SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNLQWHPATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          490      500

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAGC CGTCATTTC
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCGCGCG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAAGCGT C TATCTGTTT CACCCTATTT CGTCCCCACA AAATCCGCGC
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCGGTCCATT CCGGTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCACAACCA TGCCGTCCTT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACTG
1301 AAATGGGCGT TGTTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFN|TSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLD|LQYYIW RNDISGRLLF
101 NLVYLAAERG VVRVRL|LDN NTRGLD|DLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQ|TRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALQPEKSV YLVSPYFVPT KSGT|DALAKL VQDGIDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS  
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSAR LNTEMGVVIE SPKIAEQMER  
 451 TLADTSPEYA YRVTLDRHNR LQWHD PATRK TYPNEPEAKL WKRIA AKILS  
 501 LLPIESLL\*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLA AERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLA AERGVRVRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLALDSHPNIEVRLFPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
a987	NTRGLDDLLALDSHPNIEVRLFPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGESVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGESVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
a987	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m987.pep	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNR LQWHD PATRK					
a987	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNR LQWHD PATRK					
	430	440	450	460	470	480
	490	500	509			
m987.pep	TYPNEPEAKLWKRIA AKILSLLPIEGLLX					
a987	TYPNEPEAKLWKRIA AKILSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCggacaag ctgGATTTGG TCAAATGccg Cgtcgaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTTCGT TTATACGAAC GCCAgatgcg tggTGtcatG CAcggcgaca
401 ccgttACCGT CCGTCCTGCg ggtatggaCC GCAGGGGccg ccgcGAagg
451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAt cgAAATTGCC GTGCGCAAGC ATCATTTGCC GCAccgaTTC
751 AGTGAagcgt gtGcCAAATC CGcgaAAAA ATtccccgacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTG CGACCTTCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCA TCCCGATGTC GAGCGTTTGT GTATTGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAA
1351 ATCGAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGC GC CGGATTTT CTGTTGAA
1451 ACAAACATAC GGCTTTGTTC CGCAACCAT TGGGCCCCAC GCCCGAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGCGGACAA CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATCA
1601 AAGGCAGGCC GGATGCGGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGAAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGA AAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTCCGTGAA ATATTTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTTGT CACTTTGGAC GATATccata tgcacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGTTCG CCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDQVQLN RRGAVCAADK LDLVKCRVEA
101 HKDGFGEFVP LPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILPED KRLNQSIIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIEVLGDY ADGMEIEIA VRKHHLPFRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSQWALGVH TSFCERRADD AGRDVENWLK TYIMRDKVGE IFEGKISRGV
651 ANFGIFVTL DDIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKRRKG KS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TCGGAAAAAA ATCCCGTCC ATGTACGCAA
351 AAGCGATTTC AAAGGCCGCG TCGATTTCGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATTT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGA
751 TGGATTTTCA ACGGCATCGA CCATCCGTAC AAAGCCCAAA TCGACACCCT
801 TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTT CTGTTGAAAA
1001 ACAAGCATA CCGCTTTGTTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GTCGGTCTG TTGGGGCTTC AACTTGCGCG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCCTA
1251 CGAAGCATA CCGCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTCGGCGAA GTATTGGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGTT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCAACAT GGGGGACAGG
1651 GTTGCCGTCC GGGTCGCCCC TGCCGATTTC GATGACGGAA AAATCGATT
1701 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGCGGGGGA AAGGGAAGCC GAAAACGCC
```

1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC  
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG  
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE  
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADSGMEIEIA VRKHHLPHQF  
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK  
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS  
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK  
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK  
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK  
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPD AE LLQVMMLRSM  
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQOTYTP  
 451 KKSQALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT  
 501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR  
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKTA  
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKRKG S\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGDVTVTRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED					
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK				
g988		VRKHHLPHRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLP LVTIDGETARDFDDAVFAEK				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRMIPLMPENLSNGICSLNPDV				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPLMPENLSNGICSLNPDV				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL				
g988		ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIGNPHKAQIDTLYKL				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPD AE				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPD AE				
	390					

1401

	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
	:     :     :     :     :     :					
g988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNKRKYTP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	509
	KKSQWALGVHTSFCERRADDASRDVENWLKTYMMDKVGEVFEGKIS-GMTSFGIFVTL					
	:     :     :     :     :     :					
g988	NKSQWALGVHTSFCERRADDAGRDVENWLKTYMMDKVGEIFEGKISRGVANFGIFVTL					
	610	620	630	640	650	660
m988.pep	510	520	530	540	550	569
	GIHIDGLVHISDLGEDYFNRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
	:     :     :     :     :     :					
g988	DIHIDGLVHISDLGEDYFNRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
m988.pep	570	580	590	600	610	629
	IAGGSGRGRKVKSSASAKPAGTAGKGKPKTAAEKKTARGGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGKSKTTAEKKTARCGKVRGRGVPAAVESGKKAKKP					
	730	740	750	760	770	780
m988.pep	630	640				
	VPIKVKKRKGKSX					
g988	VPIKVKKRKGKSX					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988.seq
1  ATGAATAAAA ATATTAAATC TTAAATTTA CGGGA AAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTAAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GCGGACAAA TTGGATTGG TCAAATGCCG TGTCAGGCGC
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCCG CCGGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGG GCCGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCGCCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CGCCCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTACAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAA
1451 ACAAGCATAC CGCATTGTTT CGCAACCATT TGGGGCCAC GCCCGAAAA
1501 CTGCGCGCCT TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1601	AAGGCAGGCC	GGATGCCGAA	TTGCTGCAAG	TCATGATGTT	GCGCTCCATG
1651	CAACAGGCGG	TTTACGAACC	GCATTGCGAC	GGACACTTTC	GTCTTGCCTA
1701	CGAAGCATAC	GCCCACTTCA	CCTCGCCCAT	CCGCCGCTAT	CCCAGACTGA
1751	CCGTACACCG	CGCCATCAA	CGCGTGTGA	ATCAGCAAAC	CTACACGCCA
1801	AAAAAAGCT	GCGAGCGTT	GGCGGTGCAT	ACCTCGTTCT	GTGAGCGCCG
1851	TGCCGACGAC	GCCAGCCGCG	ACGTGGA AAA	CTGGCTGAAA	ACCTATTATA
1901	TGCGCGATAA	GGTCGGCGAA	GTATTGGAAG	GTAAAATCTC	CGGCATGACC
1951	AGTTTGGTA	TCTTTGTAAC	ACTGGACGGC	ATCCACATTG	ACGGCTTGGT
2001	GCATATCAGC	GATTTGGGCG	AAGACTATTT	CAACTCCGCG	CCCGA AATCA
2051	TGGCAATCGA	AGGCGAACGC	AGCGCATCC	GTTTCAACAT	GGGGACAGG
2101	GTTGCCGTCC	GGGTGCCCCG	TGCCGATTTG	GATGACGAAA	AAATCGATTT
2151	TGTCCTGATT	GCCGGGGGGA	GCGGCAGGGG	GCGGAAAGTT	AAATCATCCG
2201	CGTCTGCCAA	ACCGGCAGGG	ACGCGGGGGA	AAGGGAAGCC	GAAAACCGCC
2251	GCCGAGAAAA	AAACAGCCCG	AGGCGGCAAA	GTAAGGGGAA	GGGGCGCGTC
2301	TGCCGCGCGA	GAATCGAGGA	AAACGGCAAA	GAAACCGGTT	CCGATTAAGG
2351	TAAAAA ACG	GAAAGGCAAA	TCATAA		

This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

```

a988.pap
1 MNKNIKSLNL REKDFFLSRE KQRYEHPLPS REWIIELLER KGVPSKIEAL
51 VRELSIKVEE YEFFERRLLA MARDGQVLIN RRGADCAADK LDLVKCRVKA
101 HKDRFGFAVF LTPAKDGRFL LYERQMRGIM HGDIVTVRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGRFXMD RGVAILEPED KRLNQSIIVL PDGVARFKPE
201 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIETA VRKHHLPHQF
251 SEACAKAAKK IPDHVRKSDL KGRVDLRDL PVTIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAEQ RSTSVYFPRR VIMPLPENLS
351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHPTAL RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKRGRPAE LLQVMMLRSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
601 KKSQALGVH TSFCERRADD ASRDVENWLK TYYMRDKVGE VFEGKISGMT
651 SFGIVFTLDG IHDGLVHIS DLGDEYFNFR PEIMAEIER SGIRFNMGDR
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKTA
751 AEKKTARGKK VRGRGASAAA ESRKKAKKPV PIKVKRRKKG S*

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m988/a988 97.0% identity in 641 aa overlap

		10	20	30
m988.pep		TVLDIVERAQSKVVGRFYMDRGVAILEPED		
a988				
	LYERQMRGIMHGDI	VTVRPAGMDGRGR	REGTVLDIVERAQSKVVGRFX	MDRGVAILEPED
	130	140	150	160 170 180
m988.pep	40	50	60	70 80 90
	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA			
a988	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA			
	190	200	210	220 230 240
m988.pep	100	110	120	130 140 150
	VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK			
a988	VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK			
	250	260	270	280 290 300
m988.pep	160	170	180	190 200 210
	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV	:		
a988	IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFPRRVIPMLPENLSNGICSLNPHV	:		
	310	320	330	340 350 360
m988.pep	220	230	240	250 260 270
	ERLCMVCDMVVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL			
a988	ERLCVVDVMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSGGIEHPFKTIDTLYKL			

1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLLGLQLGGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSQWALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSQWALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAESRKKAKKPV					
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGSX					
a988	PIKVKKRKGSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCCGCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCCG	ACGCGTCGAC	CATCTTCTAC
151	AATCCCGCCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATT	CCGTCAACGC
201	CAACATCGTG	CTGCCCAGCA	TTCATTATGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCGTCCAA	GGTTCTAAAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTCGCAC	CCCACATTTA	CGGCGCATAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGTGACG	TCCCCTTCGG	CTCTGCCACC	GAATACGAAA
401	AAGATTCCGT	GTTGCGCCAC	AACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTCGAAC	CTGTCGCCGC	GTGGAAACTC	AACGAACGCC	ATTCCTTCGG
501	CGCAGGCATC	ATCGCCCAAC	ATAATTCCGC	CGAACTGCGC	AAATATGCCG
551	ACTGAGGAAT	CCCCAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAAT	CAAGGCCGAC	GGACACGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	CGTGGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGGCGATG	CCGAATGGGC	GGCAGACGGC	GCGGCGGCGA	AACAACAGTG
801	GAATGACAAT	ATGCTCACAC	CGCTCGTTA	CACGGCGAAT	GAAAAAGCCA
851	GTGTCAAAAT	CGTAACGCCT	GAGTCTTTGT	CCGTACACGG	CATGTACAAA

1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAAGTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGCACGCTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
1 MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNNDLTVGL GVVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAQIKAD GHADVKGSDW GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMYSK
301 VSDKADLFGD VTWTRHSRFR KAELFFFEKEK NIANGKKS DR TTITPNWRNT
351 YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
1 ATGACCCCTT CCGCACTGAA AAAAACCCTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTTCAT TATGAGCGCG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC
301 AAAATCACC AACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CCGTGTAGCC GAAGCTGCAA AAATTCAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCTTGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACATC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGCCA
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCCTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG CGCGCTTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CCGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
1 MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTPAPH IYGAYKVNND LTVGLGVYVP FGSATEYEK D SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNGVA EAAKIQADGH ADVKGS DWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMYSKVD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI  
 401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF  
 451 KNHADIIGLQ YTYKFK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

**g989/m989** 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKT	VLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----	DASTIFYNPAGL		
m989	MTPSALKKT	VLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL			
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES				
m989	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMVKVSDKADLFGDVTWTRHSRNFKAELFFEKEKNIANGKKSDRTTITPNWRNTYK				
m989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGFSGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	400
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq  
 1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT  
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG  
 101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA  
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA  
 201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG  
 251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTC GAAAAGCGGC

1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTGTC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCCTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

a989.pep

```

1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERSH FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGSWDWFGYQ LAWMWDINDR ARVGVNYSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLFQDVTWTR HSRFDKAEV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVFGF GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVDDAAYTH IHINDTSYRT AKASGNDVDS KGASSAREFN
451 HADIIGLQYT YKFK*

```

m989/a989 93.1% identity in 467 aa overlap

```

          10          20          30          40          50          60
m989.pep  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          |||
a989      MTPSALKKTVLLLGTAFAAASQASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL
          10          20          30          40          50          60

          70          80          90          100         110         120
m989.pep  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          |||
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          70          80          90          100         110         120

          130         140         150         160         170         180
m989.pep  LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
          |||
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
          130         140         150         160         170         180

          190         200         210         220         230         240
m989.pep  SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWFGYQLAWMWDI
          |||
a989      SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWFGYQLAWMWDI
          190         200         210         220         230

          250         260         270         280         290         299
m989.pep  NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
          |||
a989      NDRARVGVNYSKVSHTLKGDAEWAADDAMAKQLWDANKLALLGYTPSEKARVKIVTPES

```

1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVLVFEKEKTVVKGKSDRTTITPNWRNTYKV					
a989	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVLVFEKEKTIIVNGKSDRTTITPNWRNTYKV					
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSAREFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAAT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGCG GGTAAAAGT CAATTACAGG ATTTATACAA AACCAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCGAC GTCCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTACG
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCCTGTTT GGCTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGCGC TGGTTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCTCG
1051 CAAAATTTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
1201 GGCGGCAGGG CCGGCCAGCA CGCATCAGT AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCCTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGGAATA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACTACTT GGGCGTAAAC GGCGGCTTTA CCGACACGCA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTTCGGC AAAAACCCTT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGGCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGTA VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAACACTACA AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCG GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCCGCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTGTC GCGTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGCGCG GAAAACTGTA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGCGCGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTCTGGG
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGCAA AGGCGTGCAA ATCGGCGCGC
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGCAAT CCGGCTGATG
1201 GCGGCGAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTATTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCCTGCGG AACGCTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTGCAAGG CCGCTACAAC GCGCTGTGCG
1451 CGGAAGGCGT TGTCGGAAAA GGCAATAATG TCGGTTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGCGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCGC
1601 GCATTGCGGC AAAAAACCCG TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKKYITDLY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

```

1409

401 GGRAGQHASV NGKGGAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY  
 451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQF  
 501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ  
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG  
 601 YGKRTDGDKE AALSLKWL\*F

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKKYITDITYGDNLDKAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m990.pep	KFSTLKQTMPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m990.pep	ALTFEDKVSQSGVVLERRPENLKTLDGRKLIAAKTADSGSFAFKQNYRQGLYELLKQC					
a990	ALTFEKVSQSGVVLERRPENLKTLDGRKLIAAEKADSNSFAFKQNYRQGLYELLKQC					
	250	260	270	280	290	300
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAAADGWRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAGSD					
a990	RSHQNIRGGAAADGRRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAGSY					
	370	380	390	400	410	420
	430	440	450	460	470	480
m990.pep	LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNVRFYLQFQAQFTYLGVNNGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
a990	ALVAEGVVGKGNVRFYLQFQAQFTYLGVNNGFTDSEGTA VGLLGSGQWQSRAGIRAKTR					
	490	500	510	520	530	540
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPFPAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPFPAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

**g992.seq**

```

1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTCAG  GGGACGTGGG  TTTCGACGCG  CCCGTTCCGC  GACGGGCATC
201 GGCGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCC  TCACGTCATC  GACGCGCAGC  GCGCGAAACA  TAAATTCGG
301 ATGGCGTATA  TCGACGCACC  GGAGATGAAA  CAGGCTTACG  GTACACGTTT
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAAGTTAT  GCTAAGAAG  AGCAGGATAA  GCGGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATTCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

**g992.pep**

```

1  MFRHRHLKN  MQIKKIMKWL  PVALSLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDSVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

**m992.seq**

```

1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GTTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GCGCGGCGAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GGCGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGCGCAGC  GCGCGAAACA  CAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCGCG
401 TGTTCGATAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAAGTTAT  GCTAAGAAG  AGCAGGATAA  GCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGGCGG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

**m992.pep**

```

1  MFRHRHLKN  MQIKKIMKWL  PVALSLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFDTDRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFETDRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIWX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DSVGEWLGIWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```
a992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCT  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCGCGGCAG  GGGACGCGGG  TTCCGACGCG  CCGGCCCGCC  GCCGAGCATC
201 GGCGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGCGGGAAGG  CAGGAAAGTC  AGCGTCCCG
401 TGTTTCGACAC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAGTTAT  GCTAAAGAAC  AGCAGGATAA  GCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAGCT
601 AAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGTTG
701 AA
```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```
a992.pep
1  MFRRRHRLKN  MQIKKIMKWL  PVALSLLGAL  GYTGYGSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGD TLHVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFDTDRY  QREVAQVSVG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWM DAVGEWL  GIW*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

a992.pep    LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNQVQDGAAWHYKSYAKEQQDKADF
            |||
m992        LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNQVQDGAAWHYKSYAKEQQDKADF
            |||
            130      140      150      160      170      180

            190      200      210      220      230
a992.pep    ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIX
            |||
m992        ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIX
            |||
            190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCGC ATGGTGGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TTGCCTACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGA GCGCTGCCG CGTGCGGGAC GGGATTTTCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCCTT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGQYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVED EEADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCGC ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGA GCGCTGCCG CGAGCCGAC GGGATTTTCG
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGTCAC
601 TTCATCGCAC TGTTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVKITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EEADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*



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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			
g993	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVEITGQYLHYIAQ	MEAYQFDLAAEYLLMA			
	10	20	30	40	50	60
	70	80	90	100	110	120
m993.pep	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLLAYEQMKLAAQ	GLDALPRAGRDFAWAY			
g993	AMLIEIKSRLLLPRTTEAVEDEE	ADPRAELVRRLLAYEQMKLAAQ	GLDALPRAGRDFAWAY			
	70	80	90	100	110	120
	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQ	AWLGILSRAKHTRSHEVIKETIS	SVRAQMTAILRRLNGHG			
g993	LPLEIAAETKLPEVYIADLMQ	AWLGILSRAKHTRSHEVIQETLS	SVRAQMTAILRRLNEHG			
	130	140	150	160	170	180
	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAYVVVNFIA	LLELAKEGLVRIVQEDGFGEIRIS	LNHEGAHSDGISG			
g993	ICRFHALFNPQGAAYVIVNFIA	LLELAKEGLVGIVQEDGFGEIRIS	LNHEGAHSDGIFG			
	190	200	210	220	230	240
	249					
m993.pep	TRGGRDVF					
g993	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATCCGC	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGGCGG	CGGAATATCT	TTTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCTGCG	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTGCGGGCC	GGGATTTCGC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCGCGC
501	GCAAAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTCACGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGTTTGGTCG	GAATCGTACA
651	GGAAGTCGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAGACGG	CATTTCCGGC	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

1	LKVVLSSFGQ	PLDLLLYLIR	KQNI	DVLDIP	MVKITEQYLH	YIAQIETYQF
51	DLAAEYLLMA	AMLIEIKSRL	LLPRTETVED	EEADPRAELV	RRLLAYEQMK	
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLSILSRA	
151	KHTRSHEVIK	ETISVRAQMT	AILRRLNKHG	ICRFHDLFNP	EQGAAYVVVN	
201	FIALLELAKE	GLVGIVQEVG	FGEIRISLNH	EGAHSDGISG	TRGGRDVF*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSSFGQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			
m993	LKVVLGSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	IETYQFDLAAEYLLMA			

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	10	20	30	40	50	60
	70	80	90	100	110	120
a993.pep	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
m993	AMLEIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a993.pep	LPLEIAVEAKLPEVYITDLTQAWLSILSRAKHTRSHEVIKETISVRAQMTAILRRLNKHG					
m993	LPLEIAVEAKLPEVYITDLTQAWLGILSRAKHTRSHEVIKETISVRAQMTAILRRLNKHG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a993.pep	ICRFHDLFNPEQGAAAYVVVNFIALLELAKEGLVGVQEVGFGEIRISLNHEGAHSDGISG					
m993	ICRFHDLFNPKQGAAYVVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG					
	190	200	210	220	230	240
	249					
a993.pep	TRGGRDVFX					
m993	TRGGRDVFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TTCTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATCCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GCGGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCCAAAGT TCCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAATCATC GAAACCGTGC AAAAGGAAAA CATCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACACTG GCGCGTTGT TCGGCATT T GAGCGACCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CGCGTGGGCG GAAATTTTGG GCAATAATA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAATTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPAQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPEE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
151 PLYEDLSEFY GIPLEGGAWA EILGNNNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TGCTTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCTT
151 GCGGAATCCT ACCCGCGCA ACTGCAAAAA CTGACGGGT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCCAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACACTG GGTGCGTTGT TCGGCATT T GAGCGATCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CGCGTGGGCG GAAATTTTGG GCGATAATA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTG CCGAAGATT GAATCAATTT
601 TTGAGAAAAC AGGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPAQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLGVPHITL GALFGHLSDH  
 151 PLYEDLSEY GIPLFGGAWA EILGDNLLKS DQIHANGKGY RKFAEDLNQF  
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
g996	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
m996.pep	70	80	90	100	110	120
	LTGWNIVNGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	70	80	90	100	110	120
	LTGWNIVNGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEEQTRANIAKII					
m996.pep	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNLLKS					
g996	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGNNLLKS					
m996.pep	190	200				
	DQIHANGKGYRKFAEDLNQFLRKQGFR					
g996	190	200				
	DQIHANGKGYRKFAENLNQFLRKHGFRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCG	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCACGCAAA	CCCAAGCTTG	TGATTGTCGG	CATAGCGGCG
301	AACGACTTTC	TGCGCAAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAAATCATC	GAAACCGTGC	AGAAGGAAA	CATCCCCGCC	GTCCTCGTCG
401	GCGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATT	GAGCGATCAT
451	CCGCTGTATG	AGGATTTGTC	CGAGGAATAC	GGCATTCCGC	TGTTCCGCGG
501	CGCGTGGGCG	GAAATTTTGG	GCGATAATA	TCTGAAATCC	GACCAAAATCC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAAGATT	GAATCAATT
601	TTGAGAAAC	AGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSQAQ	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLGVPHITL	GALFGHLSDH
151	PLYEDLSEY	GIPLFGGAWA	EILGDNLLKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10	20	30	40	50	60
	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					

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```

|||||
m996      MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK
          10      20      30      40      50      60

          70      80      90      100     110     120
a996.pep   LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          |||||
m996      LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
          70      80      90      100     110     120

          130     140     150     160     170     180
a996.pep   ETVQKENIPAVLVGVPHITLGALFGHLS DHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
          |||||
m996      ETVQKENIPAVLVGVPHITLGALFGHLS DHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
          130     140     150     160     170     180

          190     200
a996.pep   DQIHANGKGYRKFAEDLNQFLRKQGF
          |||||
m996      DQIHANGKGYRKFAEDLNQFLRKQGF
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGCGG TTGTCCGCGG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGCGCATACG CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTTCAGACC
251 CCGTGCCGCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCGCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTGTCTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGG CAGCCCTTGG TCTGGGGCGC GCTCAACACG CCTTTGAAAA
551 CCGCAAGCCT GCGCGTGTGG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGcC GCGCCCGCTG ACcGGCAtg CCGAcggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAttagc GTTTCGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFRL VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGGPDT
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLVLT
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGAGG CTGTCCGCGG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGCGCATACG CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTTCGGATC
251 CCGTGCCGCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCGCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAAGTGTCTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGAAAA

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551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACGCTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGCC CGCCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGAGGCT CGGACTGCCT GAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCC GACTTGTCTG GTTGCACCG GCACCGCATC
1201 TTCCCCGCCG GCGACTACCT CCACCCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

m997.pep

```

1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVRLMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKS GSDYLLP QDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAF VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVQW LLCRGRGLP ENEVSAVISV SDRVGAFAFR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPP DLWLHRRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
	NGQHILLGAYRGVRLMKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVRLMKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
g997.pep	130	140	150	160	170	180
	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRRAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRRAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
g997.pep	190	200	210	220	230	240
	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEFALAEQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEFALADLQRLGADIRLETRVC					
	190	200	210	220	230	240
g997.pep	250	260	270	280	290	300
	RLNTLPDGKVLVNGEAFDAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
	250	260	270	280	290	300
g997.pep	310	320	330	340	350	
	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFAFR					
m997	AEPVRLPAPLTGLADGTQVQWLLCRGRL-GLPENEVSAVISVSDRVGAFAFR					
	310	320	330	340	350	

1418

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTC A TCGGCGCAGG
51  CTGGGCCGGC TTGTCCGCGC CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCCG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGTGT TCGCCTGAT GAAAACATC GGTTCAGACC
251 CCCATGCCGC CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACGTGCTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTTCG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCTTGG CCGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAGTG
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCGCTG ACCGGAATTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCGCATT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCCG GATTGTCTGT GGTTCACCG GCACCGCATC
1201 TTCCCCGCCG GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVLRMLMTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDDA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLR
301 AEPVRLPAPL TGLADGTQVW LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPD DLSWLHRHRI
401 FPA GDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

```
a997/m997 98.2% identity in 437 aa overlap

      10      20      30      40      50      60
a997.pep MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD
          |||
m997     MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD
          |||

      70      80      90     100     110     120
a997.pep NGQHILLGAYRGVLRMLMTIGSDPHAAFLRVPLHWHMHGGLOFRALPLPAPLHILGGVLL
          |||
m997     NGQHILLGAYRGVLRMLMTIGSDPRAAFLRVPLHWHMHGGLOFRALPLPAPLHILGGVLL
          |||

      70      80      90     100     110     120
a997.pep ARRVPFAFKA KLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRRAAVMQFWQPLVWGALNT
          |||
m997     ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRRAAVMQFWQPLVWGALNT
          |||

      130     140     150     160     170     180
a997.pep PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC
          |||
m997     PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC
          |||

      190     200     210     220     230     240
a997.pep PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC
          |||
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m997      PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEFPDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           |||||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRHRIFPAGDYLHPDYPATLEAAVQ
           |||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRHRIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
51 AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACCTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGTAAAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 3020; ORF 999&gt;:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QSKTAQAEV PVQSIQAADC TAPMDITVEQ
51 YLINLEQAFK TQNVSTKIHN KNIVKTDGKY DLTLMDFGA IALKLDEQK
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTTT DKLGESEAGK
151 QLFATLTVV KESNOTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.